

Delaval, Jan

91996 + 92523

From: Huynh, Phuong N.
Sent: Tuesday, April 22, 2003 8:48 AM
To: Delaval, Jan
Subject: RE: RE: 09/674,716

Good morning Jan,
The correct USSN is 09/674,716. Sorry about that. How are you doing otherwise? Neon.

-----Original Message-----

From: Delaval, Jan
Sent: Tuesday, April 22, 2003 7:10 AM
To: Huynh, Phuong N.
Subject: RE: RE: 09/555,964

no CRF for this case number

http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL_ID=09555964

-----Original Message-----

From: Huynh, Phuong N.
Sent: Monday, April 21, 2003 1:37 PM
To: Delaval, Jan
Subject: RE: 09/555,964

Jan,

Please search peptides of SEQ ID NO: 3, 5, 7, 9, 11, 13, 1, 2, 17, 18 against commercial and interference databases.

Thanks,
Neon
Art unit 1644
Mail 9E12
Tel 308-4844

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

Access DB# 91996

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

STAFF USE ONLY

Searcher: <u>Jan</u>	Type of Search <input checked="" type="checkbox"/>	Vendors and cost where applicable <input checked="" type="checkbox"/>
Searcher Phone #: <u>4448</u>	NA Sequence (#) <input checked="" type="checkbox"/>	STN <input checked="" type="checkbox"/>
Searcher Location: <u>4120/03</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog <input type="checkbox"/>
Date Searcher Picked Up: <u>4/26/03</u>	Structure (#) <input checked="" type="checkbox"/>	Questel/Orbit <input type="checkbox"/>
Date Completed: _____	Bibliographic <input type="checkbox"/>	Dr.Link <input type="checkbox"/>
Searcher Prep & Review Time: _____	Litigation <input type="checkbox"/>	Lexis/Nexis <input type="checkbox"/>
Clerical Prep Time: <u>60</u>	Fulltext <input type="checkbox"/>	Sequence Systems <input checked="" type="checkbox"/>
Online Time: <u>120</u>	Patent Family <input type="checkbox"/>	WWW/Internet <input type="checkbox"/>
	Other <input type="checkbox"/>	Other (specify) _____

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:53:31 ; Search time 828.199 seconds
(without alignments)
14583.043 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 415

Sequence: 1 aaagctttacagttactcagc.....tggggccaagggacactagt 415

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_hgt:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_hgt_hum:*

31: em_hgt_inv:*

32: em_hgt_other:*

33: em_hgt_mus:*

34: em_hgt_pin:*

35: em_hgt_rod:*

36: em_hgt_mam:*

37: em_hgt_vrt:*

38: em_sy:*

39: em_hgt_hum:*

40: em_hgt_mus:*

41: em_hgtg_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	415	100.0	415	6	AX010600	Sequence
2	415	100.0	415	6	AX010643	Sequence
3	310.6	74.8	1658	10	BC031470	Mus muscu
4	310.4	74.8	453	6	AX080317	Sequence
5	295.6	71.2	405	10	MM05819	Mus muscu
6	295.2	71.1	477	10	AB050074	Mus muscu
7	292.6	70.5	399	10	MUSIGHFZX	Mus muscu
8	289.8	69.8	396	10	MMU223543	Mus muscu
9	289	69.6	314	10	MUSIGHRT	Mus muscu
10	288	69.4	314	10	MUSIGHRU	Mus muscu
11	287.4	69.3	314	10	MUSIGHRW	Mus muscu
12	286.4	69.0	208357	2	AC073590	Mus muscu
13	284.4	68.5	313	10	MUSIGHRY	Mus muscu
14	284.2	68.5	314	10	MUSIGHRX	Mus muscu
15	283.8	68.4	345	10	MMIGM18	Mus muscu
16	283.2	68.2	306	10	MUSIGHRV	Mus muscu
17	281	67.7	314	10	MUSIGHR2	Mus muscu
18	278.6	67.1	414	10	MUSIGHAA2	Mus muscu
19	278.6	67.1	417	10	MUSIGHAAL	Mus muscu
20	278.4	67.1	305	10	MUSIGHSA	Mus muscu
21	277.2	66.8	318	10	MMHCVR	Mus muscu
22	273.6	65.9	375	10	AY090914	Mus muscu
23	273.4	65.9	417	10	MUSIGHBMA	Mus muscu
24	272.4	65.6	300	10	MMIGVH22	Mus muscu
25	272	65.5	357	6	E15671	DNA encodin
26	271.2	65.3	345	10	AF132844	Mus muscu
27	270.4	65.2	363	10	MUSIGKCLI	Mus muscu
28	269.4	64.9	403	6	AR022572	Sequence
29	269.4	64.9	403	6	AR037587	Sequence
30	269.4	64.9	403	6	AR178045	Sequence
31	269	64.8	351	10	AY090913	Mus muscu
32	268.8	64.8	351	10	S73907	ig v kappa
33	268.6	64.7	427	10	MUSIGHHT	Mus muscu
34	268.4	64.7	351	10	AF242213	Mus muscu
35	268.4	64.7	376	10	MUSBRE3A	Mus muscu
36	268.4	64.7	376	10	MMIGHVEA	Mus muscu
37	267.8	64.5	360	6	AR108682	Sequence
38	267.2	64.4	354	10	MMU73591	Mus muscu
39	266.8	64.3	185591	2	AC073561	Mus muscu
40	266.8	64.3	208357	2	AC073590	Mus muscu
41	266.2	64.1	1515	9	S65761	anti-colore
42	265.6	64.0	345	10	AF178605	Mus muscu
43	265.6	64.0	345	10	AF178606	Mus muscu
44	265.6	64.0	345	10	AF178607	Mus muscu
45	265.6	64.0	357	10	MMHCVRL0	Mus muscu

ALIGNMENTS

RESULT 1	AX010600	Sequence 1	415 bp	DNA	linear	PAT 06-SEP-2000
LOCUS	AX010600	Sequence 1 from Patent WO9958679.				
DEFINITION	AX010600					
ACCESSION	AX010600					
VERSION	AX010600.1	GI:9997411				
KEYWORDS	house mouse.					
SOURCE	Mus musculus					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
AUTHORS	1 (bases 1 to 415)					
TITLE	Bonnefoy J.Y., Crowe S.J., Rapson N.T., Ellis J.H. and Shearman J.					
JOURNAL	Antibodies to cd23, derivatives thereof, and their therapeutic uses					
	Patent: WO 9958679-A 1 18-NOV-1999;					

BONNEFOY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY (GB); SHEARIN JEAN (US)

FEATURES source

Location/Qualifiers
1. .415
/organism="Mus musculus"
/db_xref="taxon:10090"
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC07526.1"
/translation="ALOLLSTODLMDLFLFFIIVLLKGVSEVKLEBSGGGLVQPGG
SKMLSCVAGSFTEFSCVWMSVWROSPKGLWVAEIRLKDNDVATHYAESVKGKFTISR
DQSKRLYLQMSLRAESGVYCTDFDWMGGTL"

BASE COUNT

111 a 76 c 110 g 118 t
Query Match 100.0%; Score 415; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.9e-113;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES

1 AAGCTTTACAGTTACTCAGCACACAGAGACCTCACCATGGATTTTGGCTGATTTTTTA 60
|||||
Db 1 AAGCTTTACAGTTACTCAGCACACAGAGACCTCACCATGGATTTTGGCTGATTTTTTA 60
|||||
Qy 61 TTGTTCTTTTAAAGGGGTCAGAGTGAAGTGAAGCTTGAGGAGCTGGAGAGGCTTGG 120
|||||
Db 61 TTGTTCTTTTAAAGGGGTCAGAGTGAAGTGAAGCTTGAGGAGCTGGAGAGGCTTGG 120
|||||
Qy 121 TGCAACCTGGAGGATCCATGAAACTCTCTGTGTAGCCTCTGGATTTCAGTGGCT 180
|||||
Db 121 TGCAACCTGGAGGATCCATGAAACTCTCTGTGTAGCCTCTGGATTTCAGTGGCT 180
|||||
Qy 181 ACTGGATGCTTGGTCCGCGAGTCCACAGAGAGGGCTTGAGTGGTGTCTGAAATTA 240
|||||
Db 181 ACTGGATGCTTGGTCCGCGAGTCCACAGAGAGGGCTTGAGTGGTGTCTGAAATTA 240
|||||
Qy 241 GATTGAAATCTGATAATTATGCAACACATTATCGGAGTCTGTGAAAGGGAAGTTACCA 300
|||||
Db 241 GATTGAAATCTGATAATTATGCAACACATTATCGGAGTCTGTGAAAGGGAAGTTACCA 300
|||||
Qy 301 TCTCAAGAGATGATTCACAAAGTCGTCTACCTGCAATGAACAGCTTAAGAGCTGAAG 360
|||||
Db 301 TCTCAAGAGATGATTCACAAAGTCGTCTACCTGCAATGAACAGCTTAAGAGCTGAAG 360
|||||
Qy 361 ACAGTGGAGTTTATTACTGTACAGATTTCATAGACTGGGCGCCAAAGGACACTAGT 415
|||||
Db 361 ACAGTGGAGTTTATTACTGTACAGATTTCATAGACTGGGCGCCAAAGGACACTAGT 415
|||||

RESULT 2

AX010643/c
LOCUS AX010643
DEFINITION Sequence 46 from Patent WO9958679.
ACCESSION AX010643
VERSION AX010643.1 GI:9997452
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 415)
Bonnefoy J.Y., Crowe S.J., Rapson N.T., Ellis J.H. and Shearin J.
Antibodies to cd23, derivatives thereof, and their therapeutic uses
Patent: WO 9958679-A 46 18-NOV-1999;
BONNEFOY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY (GB); SHEARIN JEAN (US)

FEATURES source

1. .415
/organism="Mus musculus"
/db_xref="taxon:10090"

BASE COUNT

118 a 110 c 76 g 111 t
Query Match 100.0%; Score 415; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.9e-113;
Matches 415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES

1 AAGCTTTACAGTTACTCAGCACACAGAGACCTCACCATGGATTTTGGCTGATTTTTTA 60
|||||
Db 415 AAGCTTTACAGTTACTCAGCACACAGAGACCTCACCATGGATTTTGGCTGATTTTTTA 356
|||||
Qy 61 TTGTTCTTTTAAAGGGGTCAGAGTGAAGTGAAGCTTGAGGAGCTGGAGAGGCTTGG 120
|||||
Db 355 TTGTTCTTTTAAAGGGGTCAGAGTGAAGTGAAGCTTGAGGAGCTGGAGAGGCTTGG 296
|||||
Qy 121 TGCAACCTGGAGGATCCATGAAACTCTCTGTGTAGCCTCTGGATTTCAGTGGCT 180
|||||
Db 295 TGCAACCTGGAGGATCCATGAAACTCTCTGTGTAGCCTCTGGATTTCAGTGGCT 236
|||||
Qy 181 ACTGGATGCTTGGTCCGCGAGTCCACAGAGAGGGCTTGAGTGGTGTCTGAAATTA 240
|||||
Db 235 ACTGGATGCTTGGTCCGCGAGTCCACAGAGAGGGCTTGAGTGGTGTCTGAAATTA 176
|||||
Qy 241 GATTGAAATCTGATAATTATGCAACACATTATCGGAGTCTGTGAAAGGGAAGTTACCA 300
|||||
Db 175 GATTGAAATCTGATAATTATGCAACACATTATCGGAGTCTGTGAAAGGGAAGTTACCA 116
|||||
Qy 301 TCTCAAGAGATGATTCACAAAGTCGTCTACCTGCAATGAACAGCTTAAGAGCTGAAG 360
|||||
Db 115 TCTCAAGAGATGATTCACAAAGTCGTCTACCTGCAATGAACAGCTTAAGAGCTGAAG 56
|||||
Qy 361 ACAGTGGAGTTTATTACTGTACAGATTTCATAGACTGGGCGCCAAAGGACACTAGT 415
|||||
Db 55 ACAGTGGAGTTTATTACTGTACAGATTTCATAGACTGGGCGCCAAAGGACACTAGT 1

RESULT 3

BC031470
LOCUS BC031470
DEFINITION Mus musculus, Similar to immunoglobulin heavy chain 1 (serum Ig2a), clone MGC:25748 IMAGE:3991558, mRNA, complete cds.
ACCESSION BC031470
VERSION BC031470.1 GI:21594582
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE

1 (bases 1 to 1658)
Strausberg, R.
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amgebcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 30 Row: h Column: 18

RESULT 4					
AX080317	LOCUS	AX080317	453 bp	DNA	linear
	DEFINITION	Sequence 14 from Patent WO0105427.			
	ACCESSION	AX080317			
	VERSION	AX080317.1	GI:13159779		
	KEYWORDS				

```
/organism= Mus musculus  
/strain= "BALB/c"
```

VERSION

```
/db_xref="taxon:10090"
/chromosome="12"
/clone="VH11.1"
/cell_line="3S10/1"
/cell_type="hybridoma"
/clone_lib="3S10/1"
1..>405
/codon_start=1
/product="Ig mu heavy chain V-JH2 region"
/protein_id="AA16370.1"
/db_xref="GI:456280"
/translation="MDRLSCAFIVLLKGVQTEVILESGGLVHPGSMKLSVGS
SFESYDWVWRQSPKLEWIAEIRLKSDFATFYAESLKGRTISRDDSKSLYL
QMSLGTEDTGYYCTAGTYDYGQGTLLTSS"
1..57
sig_peptide
mat_peptide
58..>405
/product="unnamed"
58..366
V_region
367..405
J_segment
/note="JH2 region"
BASE COUNT 105 a 82 c 102 g 116 t
ORIGIN

Query Match 71.2%; Score 295.6; DB 10; Length 405;
Best Local Similarity 92.8%; Pred. No. 1.6e-77;
Matches 310; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 53 TTTTATTGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGTCTGAGAGTCTGGAGG 112
|||||
Db 24 TTTTATTGTTCTTTTAAAGGTGTCCAGACTGAAGTGAAGTCTTGGAGAGTCTGGAGG 83

Qy 113 AGCGTGGTCAACCTGGAGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTTT 172
|||||
Db 84 AGCGTGGTCAACCTGGAGATCCATGAACCTCTCTGTGTAGTCTCTCAATTACTTT 143

Qy 173 CAGTGGCTACTGGATGCTTGGGCTCGCCAGTCTCCAGAGAGGGGCTTGAGTGGGTGC 232
|||||
Db 144 CAGTGGCTACTGGATGCTTGGGCTCGCCAGTCTCCAGAGAGGGGCTTGAGTGGATGC 203

Qy 233 TGAATTAGATTGAATCTGATTAATTATGCAACATATTGCGGAGTCTGTGAAAGGGA 292
|||||
Db 204 TGAATTAGATTGAATCTGATTAATTGCAACATATTATGCGGAGTCTCTGAAAGGGAG 263

Qy 293 GTTCACATCTCAAGAGATGATCCAAAGTCTCTACCTCCAAATGAACAGCTTAAG 352
|||||
Db 264 GTTCACATCTCAAGAGATGATCCAAAGTCTCTACCTCCAAATGAACAGCTTAGG 323

Qy 353 AGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
|||||
Db 324 AACTGAAGACACTGGAATTATTACTGTACGGCT 357

RESULT 6
AB050074 477 bp mRNA linear ROD 02-APR-2002
LOCUS Mus musculus VH10G1 mRNA for anti-dsRNA (RDV-RNA) antibody, partial
DEFINITION cds.
ACCESSION AB050074
VERSION AB050074.1 GI:19909923
KEYWORDS
SOURCE Mus musculus (strain:BALB/c) cell_line:hybridoma 10G1 cDNA to mRNA.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Kitagawa,Y., Matsumoto,T., Okuhara,E. and Shikata,E.
TITLE Immunogenicity of rice dwarf virus-ribonucleic acid
JOURNAL Tohoku J. Exp. Med. 122 (4), 337-343 (1977)
MEDLINE 78034786
PUBMED 918970
REFERENCE
1 Kitagawa,Y.
2 anti-dsRNA (RDV-RNA) Ab VH region-VH10G1

JOURNAL Published Only in Database (2002)
REFERENCE 3 (bases 1 to 477)
AUTHORS Kitagawa,Y.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-2000) Yoshichika Kitagawa, Akita Prefectural
University, Biotechnology Institute; minami 2-2, Ogata, Akita
010-0444, Japan (E-mail:kitagawa@agri.akita-pu.ac.jp,
URL:www.akita-pu.ac.jp/, Tel:81-185-45-2026(ex.400),
Fax:81-185-45-2678)
FEATURES
Location/Qualifiers
source
1..477
/organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/cell_line="hybridoma 10G1"
1..477
/gene="VH10G1"
11..>475
/gene="VH10G1"
/codon_start=1
/product="anti-dsRNA (RDV-RNA) antibody"
/protein_id="BAB87186.1"
/db_xref="GI:19909924"
/translation="MYGLSCVFIVLLKGVQSEVKLEBSGGGLVDPGSMKLSVGS
GFTESYMMNMVRSPEKLEWIAEIRLKSNNYATHYAESVKGRTISRDDSKSVYL
OMNLRADETGIYCTRLVMSNRYFDYWGQGTLLTVSSESQSPFNPLVSL"
BASE COUNT 126 a 102 c 119 g 130 t
ORIGIN

Query Match 71.1%; Score 295.2; DB 10; Length 477;
Best Local Similarity 89.3%; Pred. No. 2.2e-77;
Matches 318; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 27 GACCTCACCATGGATTTTGGGCTGATTTTATTATTGTTCTTTTAAAGGGTCCAGAGT 86
|||||
Db 8 GACATGTACTTGGGACTGAGCTGTGATTCATAGTTTCTCTTAAAGGTGTCAGAGT 67

Qy 87 GAAGTGAAGCTTGAGGAGTCTGGAGAGGCTTGGTGAACCTGGAGGATCCATGAAGTCT 146
|||||
Db 68 GAAGTGAAGCTTGAGGAGTCTGGAGAGGCTTGGTGAACCTGGAGGATCCATGAAGTCT 127

Qy 147 TCCTGTGTAGCTCTGGATTTACTTTCAGTGCCTAGTGTCTTGGTCCGCGAGTCT 206
|||||
Db 128 TCCTGTGTAGCTCTGGATTTACTTTCAGTGCCTAGTGTCTTGGTCCGCGAGTCT 187

Qy 207 CCAGAGAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA 266
|||||
Db 188 CCAGAGAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATTATGCAACA 247

Qy 267 CATATGCGGAGTCTGTGAAAGGGAAGTTCCACATCTCAAGAGATGATTCCAAAGTCGT 326
|||||
Db 248 CATATGCGGAGTCTGTGAAAGGGAAGTTCCACATCTCAAGAGATGATTCCAAAGTAGT 307

Qy 327 CTCACCTGCAAAATCAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTGAGTTTACTGTAC 382
|||||
Db 308 GTCTACCTGCAAAATCAACAGCTTAAGAGCTGAAGAGCTGAGCATTATTACTGTAC 363

RESULT 7
MUSIGHFZX
LOCUS Mouse Ig family J606 active mu-chain V-J2 region anti-dextran mRNA,
DEFINITION hybridoma 58.2C10.3.
ACCESSION M17726
VERSION M17726.1 GI:195318
KEYWORDS C-region; J-region; V-region; immunoglobulin heavy chain;
immunoglobulin mu-chain; processed gene.
SOURCE Mouse (C57BL) hybridoma cell line 58.2C10.3, cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 399)
REFERENCE
1 Akolkar,P.N., Sikder,S.K., Bhattacharya,S.B., Liao,J., Gruezo,F.,
```



```

FEATURES          Location/Qualifiers
source            1. .314
                  /organism="Mus musculus"
                  /db_xref="taxon:10090"
Intron            <1..11
                  /note="Ig H-chain V-region intron"
exon              12..>314
                  /note="Ig H-chain V-region, X"
BASE COUNT       88 a 58 c 86 g 82 t
ORIGIN            Chromosome 12.

Query Match      69.6%; Score 289; DB 10; Length 314;
Best Local Similarity 95.2%; Pred. No. 1.5e-75;
Matches 298; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 76 GGGTCCAGAGTGAAGCTTGAGGAGCTTGAGGAGGCTTGGTGCAACCTGGAGGAT 135
Db 2 GGGTCCAGAGTGAAGCTTGAGGAGCTTGAGGAGGCTTGGTGCAACCTGGAGGAT 61

QY 136 CCATGAAACTCTCCTGTGAGCCTCTGGATTACTTTTCAGTGGCTACTGGATGCTTGGG 195
Db 62 CCATGAAACTCTCCTGTGAGCCTCTGGATTACTTTTCAGTGGCTACTGGATGCTTGGG 121

QY 196 TCCGCCAGTCTCCAGAGAAAGGGCTTGAGTGGTTCGCTGAAATAGATTGAAATCTGATA 255
Db 122 TCCGCCAGTCTCCAGAGAAAGGGCTTGAGTGGTTCGCTGAAATAGATTGAAATCTGATA 181

QY 256 ATTATGCAACACATTATGCGGAGTCTGTGAAAGGAAATTCACCATCTCAAGAGATGATT 315
Db 182 ATTATGCAACACATTATGCGGAGTCTGTGAAAGGAAATTCACCATCTCAAGAGATGATT 241

QY 316 CCAAAAGTCGTCTCTACCTGCACAAATGAACAGCTTAAGAGCTGAACACAGTGGATTTATT 375
Db 242 CCAAAAGTCGTCTCTACCTGCACAAATGAACAGCTTAAGAGCTGAACACAGTGGATTTATT 301

QY 376 ACTGTACAGATTT 388
Db 302 ACTGCACAGATCT 314

RESULT 11
MUSIGHRW          MUSIGHRW          314 bp      mRNA      linear      ROD 27-APR-1993
LOCUS             Mouse Ig active H-chain (GAC1) mRNA V-region, from hybridoma
DEFINITION        M32047, partial cds.
ACCESSION         M32047.1 GI:195972
VERSION           M32047.1
KEYWORDS          V-region; immunoglobulin heavy chain; processed gene.
SOURCE            Mouse (strain A/J), cDNA to mRNA, anti-GAC hybridoma 68.2C4.
ORGANISM          Mus musculus
REFERENCE          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS            Jarvis,C.D., Cannon,L.E. and Stavnezer,J.
TITLE             Mouse antibody response to group A streptococcal carbohydrate
JOURNAL            J. Immunol. 143 (12), 4213-4220 (1989)
MEDLINE           90079033
PUBMED            2512352
FEATURES          Location/Qualifiers
source            1. .314
                  /organism="Mus musculus"
                  /db_xref="taxon:10090"
Intron            <1..11
                  /note="Ig H-chain V-region intron"
exon              12..>314
                  /note="Ig H-chain V-region, X"
BASE COUNT       89 a 57 c 84 g 84 t
ORIGIN            Chromosome 12.

Query Match      69.3%; Score 287.4; DB 10; Length 314;
Best Local Similarity 94.9%; Pred. No. 4.6e-75;
Matches 297; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 76 GGGTCCAGAGTGAAGCTTGAGGAGCTTGAGGAGGCTTGGTGCAACCTGGAGGAT 135
Db 2 GGGTCCAGAGTGAAGCTTGAGGAGCTTGAGGAGGCTTGGTGCAACCTGGAGGAT 61

QY 136 CCATGAAACTCTCCTGTGAGCCTCTGGATTACTTTTCAGTGGCTACTGGATGCTTGGG 195
Db 62 CCATGAAACTCTCCTGTGAGCCTCTGGATTACTTTTCAGTGGCTACTGGATGCTTGGG 121

QY 196 TCCGCCAGTCTCCAGAGAAAGGGCTTGAGTGGTTCGCTGAAATAGATTGAAATCTGATA 255
Db 122 TCCGCCAGTCTCCAGAGAAAGGGCTTGAGTGGTTCGCTGAAATAGATTGAAATCTGATA 181

QY 256 ATTATGCAACACATTATGCGGAGTCTGTGAAAGGAAATTCACCATCTCAAGAGATGATT 315
Db 182 ATTATGCAACACATTATGCGGAGTCTGTGAAAGGAAATTCACCATCTCAAGAGATGATT 241

```

```

QY 316 CCAAAGTCGTCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTATT 375
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
Db 242 CCAAAGTAATGCTACCTCAATGAACAGCTTAAGGCTGAAGACACTGGAATTAAT 301
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
QY 376 ACTGTACAGATT 388
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
Db 302 ACTGCACAGATT 314
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||

RESULT 12
AC073590/c
LOCUS
DEFINITION
AC073590 208357 bp DNA linear HTG 13-AUG-2002
WORKING DRAFT SEQUENCE, 5 unordered pieces.
AC073590
VERSION
AC073590.4 GI:22213159
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE
house mouse.
ORGANISM
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 208357)
Smith,D.R.
Genome Therapeutics Corporation Sequencing Center: Mouse Genome
Sequence Data
Unpublished
2 (bases 1 to 208357)
Smith,D.R.
Direct Submission
Submitted (25-JUN-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
3 (bases 1 to 208357)
Smith,D.R.
Direct Submission
Submitted (13-AUG-2002) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
On Aug 13, 2002 this sequence version replaced gi:15208559.
-----
Genome Center
Center: Genome Therapeutics Corporation
Center code: GTC
Web site: http://www.genomecorp.com/
Contact: gtc-seqcenter@genomecorp.com
-----
Project Information
Center project name: mq036
-----
Summary Statistics
Sequencing vector: N/A
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 990315
Consensus quality: 205031 bases at least Q40
Consensus quality: 205605 bases at least Q30
Consensus quality: 206093 bases at least Q20
Insert size: 208000; sum-of-contigs
Quality coverage: 7.7x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1100: contig of 1100 bp in length
* 1101 1200: gap of unknown length
* 1201 2367: contig of 1167 bp in length
* 2368 2467: gap of unknown length
* 2468 3532: contig of 1065 bp in length
* 3533 3632: gap of unknown length
* 3633 29528: contig of 25896 bp in length
* 29529 29628: gap of unknown length
* 29629 208357: contig of 178729 bp in length.
*
* Location/Qualifiers

```

```

source
1. 208357
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="12"
/clone="RP23-206K17"
/clone_lib="RPCI-23"
/misc_feature
1. 1100
/note="assembly_name:Contig2"
misc_feature
1201. 2367
/note="assembly_name:Contig8"
misc_feature
2468. 3532
/note="assembly_name:Contig10"
misc_feature
3633. 29528
/note="assembly_name:Contig12"
misc_feature
29629. 208357
/note="assembly_name:Contig13"
clone_end:SP6"
BASE COUNT 60801 a 41487 c 40942 g 64723 t 404 others
ORIGIN
Query Match 69.0%; Score 286.4; DB 2; Length 208357;
Best Local Similarity 93.4%; Pred. NO. 1.2e-74;
Matches 299; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
QY 65 TCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGCTGCA 124
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
Db 187599 TGTGTTTTCAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGCTGCA 187540
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
QY 125 ACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTCTGGATTCTTTCAGTGGCTACTG 184
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
Db 187539 ACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTCTGGATTCTTTCAGTAACTACTG 187480
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
QY 185 GATGCTCTGGGTGGCCAGTCTCCAGAGAAGGGCTTGAGTGGTTCGTGGAATTAAGATT 244
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
Db 187479 GATGAATCGGGTGGCCAGTCTCCAGAGAAGGGCTTGAGTGGTTCGTGGAATTAAGATT 187420
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
QY 245 GAAATCTGATAATATGCAACACATTATGCGAGTCTGTGAAAGGGAAGTTTACCACATCTC 304
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
Db 187419 GAAATCTGATAATATGCAACACATTATGCGAGTCTGTGAAAGGGAAGTTTACCACATCTC 187360
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
QY 305 AAGAGATGATCCAAAAGTCGTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAG 364
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
Db 187359 AAGAGATGATCCAAAAGTCGTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAG 187300
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
QY 365 TGGAGTTTATTACTGTACAG 384
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||
Db 187299 TGGAAATTTATTACTGCACAG 187280
||||| | ||||| | ||||| | ||||| | ||||| | ||||| | |||||

RESULT 13
MUSIGHRY
LOCUS
DEFINITION
MUSIGHRY 313 bp mRNA linear ROD 27-APR-1993
66.4A10, partial cds.
ACCESSION
M32049
VERSION
M32049.1 GI:195974
KEYWORDS
V-region; immunoglobulin heavy chain; processed gene.
SOURCE
Mouse (strain A/J), cDNA to mRNA, anti-GAC hybridoma 66.4A10.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 313)
Jarvis,C.D., Cannon,L.E. and Stavnezer,J.
TITLE
Mouse antibody response to group A streptococcal carbohydrate
JOURNAL
J. Immunol. 143 (12), 4213-4220 (1989)
MEDLINE
90079033
PUBMED
2512352
FEATURES
Location/Qualifiers
1. 313
/organism="Mus musculus"
/db_xref="taxon:10090"
<1. .11
Intron

```


Db 121 GAGAAAGGGGCTTGAGTGGATTGCTGAAATTAGATTGAAATCTGATAATTATGCAACACAT 180
QY 270 TATGGGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCGTCTC 329
Db 181 TATGGGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCGTCTC 240
QY 330 TACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAG 384
Db 241 TACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAAATTTATTACTGTACAG 295

Search completed: April 26, 2003, 06:31:00
Job time : 871.449 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:55:21 ; Search time 549.077 Seconds
(without alignments)
12240.775 Million cell updates/sec

Title: US-09-674-716B-1
Perfect score: 415
Sequence: I aagcttcacgtactcagc.....tggggccaaggacactagt 415

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: em_estba:**
 - 2: em_esthum:**
 - 3: em_estmu:**
 - 4: em_estmu:**
 - 5: em_estov:**
 - 6: em_estpl:**
 - 7: em_estro:**
 - 8: em_estl:**
 - 9: gb_estl:**
 - 10: gb_est2:**
 - 11: gb_estc:**
 - 12: gb_est3:**
 - 13: gb_est4:**
 - 14: gb_est5:**
 - 15: em_estfun:**
 - 16: em_estom:**
 - 17: gb_gss:**
 - 18: em_gss_hum:**
 - 19: em_gss_inv:**
 - 20: em_gss_pln:**
 - 21: em_gss_vrt:**
 - 22: em_gss_fun:**
 - 23: em_gss_mam:**
 - 24: em_gss_mus:**
 - 25: em_gss_othr:**
 - 26: em_gss_pro:**
 - 27: em_gss_rod:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	296.8	71.5	914	12	BF163883
2	286.2	69.0	375	10	BB842048
3	286.2	69.0	1039	14	BQ937972
4	285	68.7	548	12	BF119726
5	284	68.4	1526	11	BC011342
6	278.2	67.0	367	10	BB842247

7	276.2	66.6	560	12	BF581663
8	273.4	65.9	597	9	AA472093
9	266	64.1	625	17	BH021344
10	247.4	59.6	615	10	BE288134
11	244.4	58.9	713	13	BG967386
12	223	53.7	904	12	BF133700
13	218.8	52.7	938	13	BG967834
14	209	50.4	522	10	AM401500
15	207.4	50.0	446	10	AW504516
16	207.4	50.0	483	10	AW402331
17	207.4	50.0	881	12	BG754897
18	207.4	50.0	898	14	BQ711108
19	205	49.4	355	12	BF116408
20	202.6	48.8	966	14	BQ711793
21	202.4	48.8	565	12	BG686641
22	200.2	48.2	900	14	BQ952498
23	199.6	48.1	934	12	BF181593
24	199.4	48.0	830	12	BG756192
25	198.8	47.9	948	12	BF663384
26	197.6	47.6	430	10	AW402433
27	196.6	47.4	780	9	AU080010
28	196.2	47.3	476	10	AW404015
29	195.8	47.2	700	12	BG757291
30	195.2	47.0	516	10	AW402430
31	194.6	46.9	932	12	BG341370
32	193.6	46.7	380	10	BB842280
33	193.6	46.7	663	10	BB586011
34	193	46.5	693	12	BG684987
35	193	46.5	866	14	BQ707524
36	192.8	46.5	865	13	BI150936
37	192.4	46.4	896	14	BQ715221
38	191.4	46.1	626	14	BM818875
39	191	46.0	864	13	BM008425
40	190.8	46.0	567	14	BQ266826
41	190	45.8	650	12	BF579925
42	189.8	45.7	452	14	BM818764
43	189.4	45.6	693	13	BG965016
44	188.6	45.4	635	12	BG398259
45	188	45.3	423	14	BM851901

ALIGNMENTS

RESULT 1
BF163883
LOCUS 601772396F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3991558 5',
DEFINITION mRNA sequence.
ACCESSION BF163883
VERSION BF163883.1 GI:11044161
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 914)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9204 row: p column: 23
High quality sequence stop: 679.
Location/Qualifiers
1. 914

FEATURES
source

Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/ Carninci, P., Shibata, Y., Hayatsu, N., M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues.		FEATURES source 1. .375 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="F430003E23" /clone_lib="RIKEN full-length enriched, 6 days neonate spleen" /tissue_type="spleen" /dev_stage="6 days neonate" /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT))-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."		BASE COUNT 107 a 69 c 99 g 100 t ORIGIN Query Match 69.0%; Score 286.2; DB 10; Length 375; Best Local Similarity 88.0%; Pred. No. 1.6e-57; Matches 323; Conservative 0; Mismatches 43; Indels 1; Gaps 1; QY 8 ACAGTACTCAGCACAGGACCTCACCATTGGCTGATTTTGGCTGATTTTATTTATTTCT 67 DB 10 ACAGGACACAGAACATTCACCATGACCTTGACATGACCTGCTTTTATTTATTTCT 69 QY 68 TTTAAAGGGTCCAGAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCC 127 DB 70 TTTAAAGGGTCCAGAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCC 129 QY 128 TGGAGATCATCAAACTCTCCTGTGTAGCTCTGATTTTACTTTTCTGCTTCTGAT 187 DB 130 TGGAGAT-CATGAAACTCTCCTGTGTAGCTCTGATTTTACTTTTCTGATTTCT 188 QY 188 GTCTTGGTCCCGACAGTCTCCAGAGAGGGGCTTGAGTGGGTTGCTGAAATTTAGATTGA 247	
/organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:3991558" /clone_lib="NCI_CGAP_Lu29" /tissue_type="spontaneous tumor, metastatic to mammary. Stem cell origin." /lab_host="DH10B" /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" 220 a 228 c 265 g 201 t		Query Match 71.5%; Score 296.8; DB 12; Length 914; Best Local Similarity 90.8%; Pred. No. 4.8e-60; Matches 327; Conservative 0; Mismatches 32; Indels 1; Gaps 1; QY 37 TGGATTTTGGGTGATTTTTTTTATTTGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGC 96 DB 60 TTGACAGTGAAGTGTGCTTTTATTTATTTGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGC 119 QY 97 TTGAGGAGTCTGGAGAGGCTTGGTGCAACCTGGAGGATCCATGAACATCTCTGTGTAG 156 DB 120 TTGAGGAGTCTGGAGAGGCTTGGTGCAACCTGGAGGATCCATGAACATCTCTGTGTAG 178 QY 157 CCTCTGGATTTACTTTCAGTGGCTACTGGATGCTTTGGTCCGCCAGTCTCCAGAGAAG 216 DB 179 CCTCTGGATTTACTTTCAGTGGCTACTGGATGCTTTGGTCCGCCAGTCTCCAGAGAAG 238 QY 217 GGCTTCAGTGGGTGCTGAAATTTAGATTTGAATCTGATAATTTATGCAACATTTATGCGG 276 DB 239 GGCTTCAGTGGGTGCTGAAATTTAGATTTGAATCTGATAATTTATGCAACATTTATGCGG 298 QY 277 AGTCTCTGAAGGAGTTCACCATCTCAAGAGATGATTCCAAAGTGGTCTCTACCTGC 336 DB 299 AGTCTCTGAAGGAGTTCACCATCTCAAGAGATGATTCCAAAGTGGTCTCTACCTGC 358 QY 337 AAATGACAGCTTAAAGAGCTGAAGCAGTGGAGTCTTATTTACTGTACAGATTTTCATAGACT 396 DB 359 AAATGACAGCTTAAAGGCTGAAGCAGTGGAGTCTTATTTACTGTACAGATTTTCATAGACT 418 RESULT 2 BB842048 375 bp mRNA linear EST 21-NOV-2001 LOCUS BB842048 RIKEN full-length enriched, 6 days neonate spleen Mus DEFINITION musculus cDNA clone F430003E23 5', mRNA sequence. ACCESSION BB842048 VERSION BB842048.1 GI:17042779 KEYWORDS EST. SOURCE house mouse. ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 375) Akinura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toyota, Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (AKimura, T., et al. 2001) Unpublished (2001) Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan			

BASE COUNT ORIGIN	263 A 263 C 257 G 242 U 14 OTHERS
Query Match Best Local Similarity Matches 303; Conservative 0;	Score 286.2; DB 14; pred. No. 1.5e-57; Mismatches 28; Indels 0; Gaps 0;
Qy 52 TTTTTTTTATTGTCCTTTTAAAGGGGTCCAGAGTGGAAGCTTGAGAGCTCGAG 111 Db 81 TATTCATAGTTTTTCTCTAAGAGGTGCCAGAGTGAAGTAAAACCTTGAGAGGCCTGAG 140 Qy 112 GAGGCTTGTCGAACCTCGAGGATCCATGAACCTCCTCTGTACTGCCCTCGATTACTT 171 Db 141 GAGGCTTGTCGARACCTGGAGATCCATGAACCTCCTCTGTCTGCCCTCGATTACTT 200 Qy 172 TCAGTGGCTACTGGATGTCCTTTGGGTCGCCCACTCTCCAGAAGGGGCTTGAGTGGGTTG 231 Db 201 TCAGTAATTACTGGATGAACCTGGGTTCGCCCACTCTCCAGAAGGGGCTTGAGTGGGTTG 260	

```

Db 144 TCACCTAAGTACATGAACCTGCGGTCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTG 203
Qy 232 CTGAATTTAGATTGAATCTGATTAATATGCAACACACATTAATGCGGAGTCTGTGAAAGGGA 291
Db 204 CTGAATTTAGATTGAATCTGATTAATATGCAACACATTAATGCGGAGTCTGTGAAAGGGA 263
Qy 292 AGTTACCATCTCAAGAGATGATTCCTCAAAAGTCTCTACCTGCGCAATGAACAGCTTAA 351
Db 264 GGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCTCTACCTGCGCAATGAACAGCTTAA 323
Qy 352 GAGCTGAAGACAGTGGAGTTTATTACTGTA-----CAGATTTCATAGACTGGGGCCCAAGG 406
Db 324 GAGTTGAAGACACTGGCATTTATTACTGTACCGAGGCTGGGTTTGCCTTACTGGGGCCCAAGG 383
Qy 407 GACACTAGT 415
Db 384 GACTCTGCT 392

RESULT 5
BC011342
LOCUS
DEFINITION Mus musculus, clone IMAGE:3992829, mRNA.
ACCESSION BC011342
VERSION BC011342.1 GI:15030173
KEYWORDS HTC.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Strausberg,R.
Direct Submission
Submitted (25-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NTH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabps-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: ang@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK plate: 23 Row: n Column: 19
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, similarity but not identity to protein
This clone has the following problem: incomplete processing.
Location/Qualifiers
1. .1526
/organism="Mus musculus"
/db_xref="taxon:10090"
/map="C57BL/6J"
/clone="IMAGE:3992829"
/tissue_type="Mammary
old, gross tissue."
/clone_lib="NCI CGAP_Mam5"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
374 a 412 c 389 g 351 t

BASE COUNT
ORIGIN

```

```

Query Match 68.4%; Score 284; DB 11; Length 1526;
Best Local Similarity 87.6%; Pred. No. 4.9e-57;
Matches 324; Conservative 0; Mismatches 40; Indels 6; Gaps 1;

Qy 52 TTTTCTTTTATTGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 111
Db 35 TATTCATAGTTTCTCTTTAAAGGGTGTCCAGAGTGAAGTGAAGTGAAGTGAAGTCTGGAG 94
Qy 112 GAGGCTTGCTGCAACCTCGAGGATCCATGAACCTCTCCTGTGTAGCCTCTGATTTACTTT 171
Db 95 GAGGCTTGCTGCAACCTCGAGGATCCATGAACCTCTCCTGTGTAGCCTCTGATTTACTTT 154
Qy 172 TCAGTGGTACTGGATGTTCTTGGTCCGCGCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTG 231
Db 155 TCCTAACTACTACTAGTAACCTGGTCCGCGCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTG 214
Qy 232 CTGAATTTAGATTGAATCTGATAATTATGCAACACATTTATGCGGAGTCTGTGAAAGGGA 291
Db 215 CTGAATTTAGATTGAATCTGATAATTATGCAACACATTTATGCGGAGTCTGTGAAAGGGA 274
Qy 292 AGTTACCATCTCAAGAGATGATTCCTCAAAAGTCTCTACCTGCAAAATGAACAGCTTAA 351
Db 275 GGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCTCTACCTGCAAAATGAACAGCTTAA 334
Qy 352 GAGCTGAAGACAGTGGAGTTTATTACTGTA-----CAGATTTCATAGACTGGGGCCCAAG 405
Db 335 GAGTTGAAGACACTGGCATTTATTACTGTACCAGGGCTGGGTTTCTTACTTGGGGCCCAAG 394
Qy 406 GCACACTAGT 415
Db 395 GGACTCTGCT 404

RESULT 6
BB842247
LOCUS
DEFINITION BB842247 RIKEN full-length enriched, 6 days neonate spleen Mus
musculus cDNA clone F430004H07 5', mRNA sequence.
ACCESSION BB842247
VERSION BB842247.1 GI:17042978
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura

```

S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicephillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
 e mouse tissues.

FEATURES

source
 1. .367
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="F430004H07"
 /clone_lib="RIKEN full-length enriched, 6 days neonate spleen"
 /tissue_type="spleen"
 /dev_stage="6 days neonate"
 /note="vector: pSPORT1; Site_1: Sali; Site_2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT) -Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
 Mol Genet 7: 1967-1978."

 BASE COUNT 105 a 68 c 98 g 96 t
 ORIGIN

Query Match 67.0%; Score 278.2; DB 10; Length 367;
 Best Local Similarity 87.7%; Pred. No. 1.3e-55;
 Matches 315; Conservative 0; Mismatches 43; Indels 1; Gaps 1;
 QY 8 ACAGTTACTCAGCACAGGACCTCACCATGGATTTTGGCGCTGATTTTATTATTGTTCT 67
 DB 10 ACAGGGACAAGACATTCACCATGGACTTGAGACTGAGCTGTGCTTTATTATTGTTCT 69
 QY 68 TTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGAGCTTGAGAGGCGTTGGTGAACC 127
 DB 70 TTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGAGCTTGAGAGGCGTTGGTGAACC 129
 QY 128 TGGAGGATCATGAACCTCTCCTGTAGCCTCTGGATTTTACCTTTCAGTGGCTACTGGAT 187
 DB 130 TGGAGGATCATGAACCTCTCCTGTGCTCTGGATTTTACCTTTCAGTGGCTACTGGAT 188
 QY 188 GTCTTGGTCCGCGAGTCTCCAGAGAAGGGCTTGAGTGGTGTGCTGAATAGATTGAA 247
 DB 189 GAATGGGTCCGCGAGTCTCCAGAGAAGGGCTTGAGTGGTGTGCTGAATAGATTGAA 248
 QY 248 ATCTGATAATTATGCAACACATATTGCGGAGTCTGTGAAAGGGAAGTTCACCATCTCAAG 307
 DB 249 ATCTGATAATTATGCAACACATATTGCGGAGTCTGTGAAAGGAGGTTTACCAATCTCAAG 308
 QY 308 AGATGATTCAAAAGTCGTCTTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTG 366
 DB 309 AGATGATTCAAAAGTAGTGTCTACCTGCAAAATGAACAACTTAAGGGCTGAAGACACTG 367

RESULT 7

BF581663
 LOCUS
 DEFINITION
 mRNA sequence.
 602099628F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4219447 5',
 560 bp mRNA linear EST 12-DEC-2000
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 560)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLAN9801 row: h column: 08
 High quality sequence stop: 555.
 Location/Qualifiers
 1. .560
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone_lib="IMAGE:4219447"
 /clone_lib="NCI_CGAP_Co24"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
 BASE COUNT 152 a 128 c 133 g 147 t
 ORIGIN

Query Match 66.6%; Score 276.2; DB 12; Length 560;
 Best Local Similarity 90.0%; Pred. No. 3.6e-55;
 Matches 307; Conservative 0; Mismatches 33; Indels 1; Gaps 1;
 QY 52 TTTTATTTTATTGTTCTTTTAAAGGGTCCAGAGTGAAGCTTGAGGAGTCTGGAG 111
 DB 82 TATTCATAGTTTCTCTTTAAAGGGTGTCCAGAGTGAAGCTTGAGGAGTCTGGAG 141
 QY 112 GAGGCTTGGTCAACCTCGAGGATCCATAAAGTCTCCTGTCTAGCCCTCGATTACTT 171
 DB 142 GAGG-TTGTGCAACCTCGAGGATCCATAAAGTCTCCTGTCTAGCCCTCGATTACTT 200
 QY 172 TCAGTGGCTACTGGATGCTTGGGTCGCGAGTCTCCAGAGAAGGGGTTGAGTGGGTTG 231
 DB 201 TTAGCAACTACTGGATGACCTGGTCCGCGACTCTCCAGAGAAGGGGTTGAGTGGATTG 260
 QY 232 CTCGAATTAAGATTGAATCTGATAATTATGCAACACATTATCCGGAGTCTGTGAAGGGA 291
 DB 261 CTGAATTAATTAAGATTGATCTGATAATTTTGAACACATTATCGGAGTCTGTGATAGGA 320
 QY 292 AGTTCCACCATCTCAAGAGATGATTTCCAAAAGTCTCTTACCTGCAAAATGAACACTTAA 351
 DB 321 GGTTCACCATCTCAGAGATGATTTCCAAAAGTAGTGTCTTACCTGCAAAATGAACACTTAA 380
 QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTACAGATTTTCATA 392
 DB 381 GAGCTGAAGACACTGGCTTTTATTACTGTACGGGTCTACTA 421

RESULT 8


```

QY 112 GAGCTTGGTGCACCTGGAGGATCCATGAAACTCTCCCTGTAGCTCTGGATTACATT 171
Db 139 GAGCTTTGGTGCACCTGGAGGATCCATGAAACTCTCCCTGTAGCTCTGGATTACATT 198
QY 172 TCAGTGGCTACTGGATCTCTTGGTCCGCCAGTCTCCAGAGAAGGGCTTGGATGGGTG 231
Db 199 TCATAACTACTGGATGAACCTGGTCCGCCAGTCTCCAGAGAAGGGCTTGGATGGGTG 258
QY 232 CTGAATATAGATTGAATCTGATAATATATGCAACACATTATGGGAGTCTGTGAAAGGGA 291
Db 259 CTGAAGTTAGATTGAATCTTAATAATATATGCCACACATTATGGGAGTCTGTGAAAGGGA 318
QY 292 AGTTCACCATCTCAAGAGATGATTCAAAAGTCTCTACCTGCAAAAT---GAACAGCT 348
Db 319 GGTTCACCATCTCAAGAGATGATTCAAAAGTCTCTACCTGCAAAATTTGAACCAACT 378
QY 349 TAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
Db 379 TAGAAGTGAAGACACTGGGTTTATATCTGTGC 412

RESULT 12
LOCUS BF133700 904 bp mRNA linear. EST 24-OCT-2000
DEFINITION 601778606F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4008801 5',
mRNA sequence.
ACCESSION BF133700
VERSION BF133700.1 GI:10972740
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 904)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9238 row: 1 column: 02
High quality sequence stop: 680.
Location/Qualifiers
1. .904
/organism="Mus musculus"
/strain="CZECB II"
/db_xref="taxon:10090"
/clone="IMAGE:4006801"
/clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 233 a 217 c 243 g 210 t
ORIGIN
Query Match 53.7%; Score 223; DB 12; Length 904;
Best Local Similarity 79.0%; Pred. No. 1.3e-42;
Matches 290; Conservative 0; Mismatches 75; Indels 2; Gaps 2;

QY 10 AGTTACTACACACAGGACCTCACCATGGATTTGGCTGATTTTTTTTATGTTCTTT 69
Db 2 AGTGACACAGACCATTCACCATGTACTTGGAGCTGTGATTATTCATGCTTTTCTCT 61

```

```

QY 70 TAAAGGGGTCAGAGTGAAGTGAAGCTTGAAGAGCTCTGGAGGAGGCTTGGTGAACCTG 129
Db 62 TAAAGGTCGTCCAGTGTGAGGTGAAGCTGAGTCTGGTGGAGCTTGGTGAACCTG 121
QY 130 GAGGATCCATGAATCTCTCTGTAGCTCTGGATTTTACATTTTCACTGGCTACTGGATGT 189
Db 122 GGAGTCCATGAATCTCTCTGTGTGT-CCCTCTGGATTCACTTTGTAGTACTA-TGGATGA 179
QY 190 CTTGGGTCGGCCAGTCTCCAGAGAAGGGCTTGAAGTGGTTCCTGAAATTAGATTGAAT 249
Db 180 ACTGGGTCACCAGTCTCCAGAGAAGGAGCTGGAGTGGGTAGCACAAATTAGAACAAAC 239
QY 250 CTGATAATATGCAACACATTATGGGAGTCTGTGAAAGGAAAGTTTACCATCTCAGAG 309
Db 240 CTTATAATATGTTACATATTATTTCAGATTCTGTGAGAGGAGATTTACCATCTCAAG 299
QY 310 ATGATTCCAAAAGTCGTCTACCTGCAAAATGAACAGCTTAAGAGCTGAACACAGTGGAG 369
Db 300 ATGATTCCAAAAGTAGTGTCTACCTGCAAAATGAACACTTAAAGAGCTGAACACAGGGA 359
QY 370 TTTATTA 376
Db 360 TCTATTA 366

RESULT 13
LOCUS BG967834 938 bp mRNA linear EST 12-JUN-2001
DEFINITION 602832666F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4986976 5',
mRNA sequence.
ACCESSION BG967834
VERSION BG967834.1 GI:14355471
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 938)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10997 row: d column: 17
High quality sequence stop: 607.
Location/Qualifiers
1. .938
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4986976"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 262 a 232 c 232 g 212 t
ORIGIN
Query Match 52.7%; Score 218.8; DB 13; Length 938;
Best Local Similarity 83.7%; Pred. No. 1.2e-47;
Matches 298; Conservative 0; Mismatches 41; Indels 11; Gaps 4;

QY 52 TTTTATTTTATTGTTCTTTTAAAGGGGCCAGAGTGAAGTGAAGCTCAAGCTCAGAGTCTGAG 111
Db 111

```

```

Db 81 TATTATAGTTTTTCTCTTAAAGGTGTCAGAGTGAAGTGAAGCTGGAGTCTGGAG 140
QY 112 GAGCTTGGTGAACCTGGAGGATCCATGAACCTCTCCTGTAGCTCTGGATTTACTT 171
Db 141 GAGCTTGGTGAACCTGGAGGATCCATGAACCTCTCCTGTAGCTCTGGATTTACTT 200
QY 172 TCAGTGGCTACTGGATGCTTTGGTCCGCCAGTCTCCAGAGAAGGGCTTTAGTGGGTTG 231
Db 201 TCAGTAACTACTGGATGAACCTGGTCCGCCAGTCTCCAGAGAAGGGCTTTAGTGGGTTG 260
QY 232 CTGAAA--TTAGATTGAATCTGATAATTA---TGCACACATTATGCGGAGTCTGTGA 285
Db 261 CTGAACCTTACGATTGAACACTCTAATAATTAATGCAACACATTATGCGGAGTCTGTGA 320
QY 286 AAGGGAATTCACCATCTCAAGAGATG--ATTCCAAAGTCGTCTTACCTGCAAAATGAA 343
Db 321 AAGGAGGTTTCAACATCTCAGAGATGCAATCCAAACAGTAGTGTCTACCTGCACATGAA 380
QY 344 CAGCTTAA---GAGCTGAAGACAGTGGAGTTTATTTACTGTACAGATTTTCATAGACT 396
Db 381 CAAGCTTAACGACGCTGAAGACACTGGCATTTATTTACTGTACAGAGGATGGACT 436

RESULT 14
AW401500          522 bp      mRNA      linear      EST 16-FEB-2000
LOCUS
DEFINITION
UI-HF-BKO-aau-b-08-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3055046 5', mRNA sequence.
ACCESSION
AW401500
VERSION
AW401500.1 GI:6920108
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 522)
REFERENCE
AUTHORS
NTH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
FEATURES
Location/Qualifiers
source
1..522
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3055046"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: p7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT
123 a 128 c 155 g 116 t
ORIGIN
Query Match 50.4%; Score 209; DB 10; Length 522;
Best Local Similarity 76.0%; Pred. No. 2.7e-39;
Matches 273; Conservative 0; Mismatches 80; Indels 6; Gaps 1;

QY 30 CTCACCATGGATTTGGGCT-----GATTTTTTTTATGTTCTTTTAAAGGGTCCAG 83

```

```

Db 70 CTCACCATGGATTTGGGCTGAGCTGAGTTTCCCTTGCTGCTATTTTAAAGGTTCCAG 129
QY 84 AGTGAAGTCAACCTTTGAGGAGTCTGGAGAGGCTTTGGTGCAACCTGGAGGATCCATGAAA 143
Db 130 TGTGAGGTGCACCTGTTGAGTCTGGGGAGGCTTGGTAAAGCCTGGGGGTCCTCTAGA 189
QY 144 CTCTCCTCTGTAGCCTCTGGATTTACTTTCTAGTGGCTACTGGATGCTTTGGTCCGCCAG 203
Db 190 CTCTCCTGTGCAGCCTCTCTGGATTTCACTTTCAGTAAACGCTGATGAGTGGTCCGCCAG 249
QY 204 TCTCCAGAGAAAGGGCTTCACTGGCTGCTGAAATAGATTGAAATCTGATAATTTATGCA 263
Db 250 GTCTCAGGAAAGGGCTTGGAGTGGTGGCCGTATTAAAGCAAACTGATGGTGGGACA 309
QY 264 ACACATTATGCGGAGTCTCTGAAAGGAAGTTTCACCATCTCAAGAGATGATTTCCAAAAGT 323
Db 310 ACAGACTACGCTGCACCCGCTGAAGAGCAGATTCACCATCTCAAGAGATGATTTCAAAAAC 369
QY 324 CGTCTCTACTCGAAATGAACAGCTTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
Db 370 ACGCTCTATCTGCAAAATGAACAGCCTGAAAACCGAGGACACAGCCGTGTATTACTGTAC 428

RESULT 15
AW504516          446 bp      mRNA      linear      EST 02-MAR-2000
LOCUS
DEFINITION
UI-HF-BNO-alj-c-03-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone
IMAGE:3079684 5', mRNA sequence.
ACCESSION
AW504516
VERSION
AW504516.1 GI:7142183
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 446)
REFERENCE
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
FEATURES
Location/Qualifiers
source
1..446
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3079684"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: p7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(3.5-4.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT
110 a 104 c 126 g 106 t
ORIGIN
Query Match 50.0%; Score 207.4; DB 10; Length 446;
Best Local Similarity 75.8%; Pred. No. 6.4e-39;
Matches 272; Conservative 0; Mismatches 81; Indels 6; Gaps 1;

```

```
Qy 30 CTCACCATGGATTTGGGCT-----GATTTTTTTTATTGTTCTTTTAAAGGGTCCAG 83
Db 70 CTCACCATGGAGTTTGGGCTGAGCTGGATTTTCCTTGTCTGCTATTTTAAAGGTGTCCAG 129
Qy 84 AGTGAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAA 143
Db 130 TGTGAGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCTGGGGGTCCCTTAGA 189
Qy 144 CTCTCCTGTGTAGCCTCTGGATTACTTTCACTGGGCTACTGGATGCTTTGGGTCCGCCAG 203
Db 190 CTCTCCTGTGCAGCCTCTGGTTTCACTTTCAATAAGCCCTGGATGAACCTGGGTCCGCCAG 249
Qy 204 TCTCCAGAGAAGGGGCTTGAGTGGTGTCTGAATTAGATTGAAATCTGATATATTATGCA 263
Db 250 GCTCCAGGGAAGGGGCTGGAGTGGGTTGGCCGTATTAAAGCAAAACTGATGGTGGGACA 309
Qy 264 ACACATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATCCAAAAGT 323
Db 310 ACAGACTACGCTGCACCCGTGAAGGCAGATTTCACCATCTCAAGAGATGATTCATAAACC 369
Qy 324 CGTCTCTACCTGCAATGAACAGCTTAAAGAGCTGAAGAGTGGAGTTTATTACTGTAC 382
Db 370 ACGTCTTATCTGCAATGAACAGCCTGAAAACCGAAGACACACAGCCCGTGTATTACTGTAC 428
```

Search completed: April 26, 2003, 07:26:36
Job time : 557.077 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:50:01 ; Search time 83.4911 Seconds

(without alignments)
11193.756 Million cell updates/sec

Title: US-09-674-716B-1
Perfect score: 415
Sequence: 1 aagctttacagtactcagc.....tggggccaaggacactagt 415

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues 4370478
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : N_Geneseq_101002.*
1: /SID2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SID2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SID2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SID2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SID2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SID2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SID2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SID2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SID2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SID2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SID2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SID2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SID2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SID2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SID2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SID2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SID2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SID2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SID2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SID2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SID2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	415	100.0	415	21	AAZ34745	Mouse anti-CD23 MA
2	310.4	74.8	453	22	AAF27975	Murine PSCA antibo
3	310.4	74.8	453	24	ABK09984	Mouse heavy chain
4	301.4	72.6	1774	20	AAZ20419	Antibody ABX-CBL h
5	293.6	70.7	496	20	AAV71155	Coding strand for
6	293.6	70.7	497	11	AAQ08605	Br-3 Heavy chain v
7	293.6	70.7	497	18	AAT43437	Mab Br-3 heavy cha
8	289.4	69.7	480	15	AAQ85388	Mab 4197X heavy ch
9	282.2	68.0	469	12	AAQ12060	Sequence encoding

10	282.2	68.0	469	12	AAQ12016	Sequence encoding
11	272	65.5	357	19	AAV22331	Nucleic acid encod
12	271.6	65.4	856	22	AAC90472	Antibody 33F12 cat
13	269.8	65.0	1979	16	AAQ85386	Anti-catacract immu
14	269.4	64.9	403	15	AAQ62750	Murine BrE-3 immu
15	269.4	64.9	403	15	AAQ62750	Murine BrE-3 immu
16	268.6	64.7	498	12	AAQ11969	Sequence encoding
17	267.8	64.5	360	18	AAQ11969	Lead binding Mab 4
18	267.2	64.4	366	21	AAQ11969	P5-11 single chain
19	265.4	64.0	765	24	AAQ38896	Encodes VH region
20	265.2	63.9	809	14	AAQ34841	SM3 heavy chain va
21	265	63.9	350	20	AAC31971	Mouse antibody 38C
22	263.6	63.5	899	22	AAC90471	Humanised murine B
23	263	63.4	403	15	AAQ62791	P5-2 single chain
24	262.4	63.2	768	24	AAQ62791	3B10xP5-2 bispecif
25	262.4	63.2	1509	24	AAQ62791	Plasmid pTERMSC2H1
26	260.6	62.8	5227	18	AAQ79537	113F1 hybridoma VH
27	259	62.4	342	21	AAQ38900	Lead binding Mab 7
28	256.6	61.8	357	18	AAT58262	Humanised CA2 heav
29	256	61.7	357	18	AAT87442	Coding sequence fo
30	256	61.7	357	19	AAV03616	cDNA encoding heav
31	256	61.7	357	20	AAQ81706	Mouse heavy chain
32	256	61.7	357	22	AAQ81893	DNA encoding anti-
33	256	61.7	357	22	AAH78593	Chimeric antibody,
34	256	61.7	357	24	AAI72610	Humanised anti-CD2
35	255.4	61.5	1335	21	AAQ34748	Nucleotide sequenc
36	254.4	61.3	357	22	AAI65696	Anti-dansyl single
37	244.4	58.9	345	14	AAQ40046	Monoclonal antibody
38	243.2	58.6	782	16	AAQ86755	Human H chain V re
39	238.4	57.4	387	17	AAQ74066	Murine anti-CA19-9
40	232.8	56.3	345	19	AAV35191	Sequence encoding
41	232.6	56.0	741	22	AAQ80824	CC49 VL / 217 / 4-
42	229.4	55.3	738	14	AAQ43293	DNA encoding a pro
43	229.4	55.3	738	15	AAQ66841	Fusion polypeptide
44	229.4	55.3	738	20	AAQ04747	
45	229.4	55.3	738	20	AAV99764	

ALIGNMENTS

RESULT 1
AAZ34745
ID AAZ34745 standard; cDNA; 415 BP.

AC AAZ34745;

XX 15-FEB-2000 (first entry)

DT Mouse anti-CD23 Mab C11 heavy chain variable region cDNA.

DE CD23; FCER1; IgE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes;
KW B-cell malignancy; therapy; ds.

OS Mus musculus.

XX Key Location/Qualifiers
CDS 3..413
/*tag= a

XX WO958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB01434.

PF

QY 232 CTGAATTTAGATTGAATCTGATATATGCAACACATTATGCGGAGTCTGTGAAAGGGA 291
 |||||
 Db 271 CTGAATTTAGATTGAATCTGATATATGCAACACATTATGCGGAGTCTGTGAAAGGGA 330
 |||||
 QY 292 AGTTCCACATCTCAAGAGATGATTCACAAAGTCGTCTTACCTGCTCAAAATGAACAGCTTAA 351
 |||||
 Db 331 GGTTCACCATCTCAAGAGATGATTCACAAAGTAGTGTCTACCTGCAAAATGAACACTTAA 390
 |||||
 QY 352 GAGCTGAACACAGTGGAGTTTATTACTGTACA 383
 |||||
 Db 391 GAGCTGAACACACTGGCATTTTATTACTGTACA 422
 |||||

RESULT 6
 ID AAQ08605 standard; DNA; 497 BP.
 AC AAQ08605;
 XX
 DT 04-MAR-1993 (first entry)
 XX
 DE Br-3 Heavy Chain V Region (mouse).
 XX
 KW Monoclonal antibody; chimera; light; heavy; chain; constant;
 KW variable; antigen; diagnosis; cancer; tumour; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 70..495
 FT /*tag= a
 XX
 PN W09002569-A.
 XX
 PD 22-MAR-1990.
 XX
 PF 06-SEP-1989; 89WO-US03852.
 XX
 PR 06-SEP-1988; 88US-0240624.
 PR 08-SEP-1988; 88US-0241744.
 PR 13-SEP-1988; 88US-0243739.
 PR 04-OCT-1988; 88US-0253002.
 PR 19-JUN-1989; 89US-0367641.
 PR 21-JUL-1989; 89US-0382768.
 XX
 PA (ITGE-) INT GENETIC ENG INC.
 XX
 PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
 XX
 DR WPI; 1990-115825/15.
 DR P-PSDB; AAR09423.
 XX
 PT Chimeric mouse-human antibodies - prepd. using genes coding for
 PT constant human region murine variable region, esp. to 3 tumour
 PT antigen
 XX
 PS Claim 13; Page 123 + Fig 15; 173pp; English.
 XX
 CC Shown is the nucleotide sequence from the end of the oligo-dC tail
 CC to the Jh3-Chl junction. The sequence is used in the prodn. of a
 CC chimeric antibody mol. comprising two light chains and two heavy chains,
 CC each having a constant region (human) and a variable region (murine)
 CC having specificity to an antigen bound by murine monoclonal antibody
 CC (MAB) Br-3. The chimeric antibodies can be used for any purpose for
 CC which the original murine MABs can be used, with the advantage that
 CC they are more compatible with the human body. They are esp. used for
 CC the diagnosis and treatment of cancer.
 XX
 SQ Sequence 497 BP; 141 A; 106 C; 118 G; 132 T; 0 other;
 Query Match 70.7%; Score 293.6; DB 11; Length 497;
 Best Local Similarity 92.8%; Pred. No. 2.3e-78;
 Matches 308; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 52 TTTTATTATTGTTCTTTTAAAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 111
 |||||
 Db 92 TATTCATAGTTTCTCTTAAAGGTGTCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 151
 |||||
 QY 112 GAGGCTTGTGCAACCTGGAGATCCATGAACCTCTCCTGTGTAGCCTCTGGATTACTT 171
 |||||
 Db 152 GAGGCTTGTGCAACCTGGAGATCCATGAACCTCTCCTGTGTAGCCTCTGGATTACTT 211
 |||||
 QY 172 TCAGTGGCTACTGATGCTTGGTCCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGTG 231
 |||||
 Db 212 TCAGTAACTATGTGATGAAGTGGTCCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGTG 271
 |||||
 QY 232 CTGAATTTAGATTGAATCTGATATATGCAACACATTATGCGGAGTCTGTGAAAGGGA 291
 |||||
 Db 272 CTGAATTTAGATTGAATCTGATATATGCAACACATTATGCGGAGTCTGTGAAAGGGA 331
 |||||
 QY 292 AGTTCCACATCTCAAGAGATGATTCACAAAGTCGTCTTACCTGCTCAAAATGAACAGCTTAA 351
 |||||
 Db 332 GGTTCACCATCTCAAGAGATGATTCACAAAGTAGTGTCTACCTGCAAAATGAACACTTAA 391
 |||||
 QY 352 GAGCTGAACACAGTGGAGTTTATTACTGTACA 383
 |||||
 Db 392 GAGCTGAACACACTGGCATTTTATTACTGTACA 423
 |||||

RESULT 7
 AAT43437
 ID AAT43437 standard; CDNA; 497 BP.
 XX
 AC AAT43437;
 XX
 DT 12-FEB-1997 (first entry)
 XX
 DE MAb Br-3 heavy chain variable region CDNA.
 XX
 KW Chimeric antibody; monoclonal antibody; Br-3; antibody engineering;
 KW tumour; antigen; breast carcinoma; lung carcinoma; colon carcinoma;
 KW ovary carcinoma; cancer; diagnosis; therapy; heavy chain; ss.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 70..497
 FT /*tag= a
 FT /product= Br-3 heavy chain V region
 XX
 EN US5576184-A.
 XX
 PD 19-NOV-1996.
 XX
 PF 06-SEP-1988; 88US-0240624.
 XX
 PR 06-MAY-1991; 91US-0659401.
 PR 06-SEP-1988; 88US-0240624.
 PR 08-SEP-1988; 88US-0241744.
 PR 13-SEP-1988; 88US-0243739.
 PR 04-OCT-1988; 88US-0253002.
 PR 19-JUN-1989; 89US-0367641.
 PR 21-JUL-1989; 89US-0382768.
 PR 27-DEC-1994; 94US-0364001.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
 XX
 DR WPI; 1997-011249/01.
 DR P-PSDB; AAW06212.
 XX
 PT Chimeric mouse-human antibodies - recognise a human tumour antigen,
 PT used for the treatment and diagnosis of human cancers
 XX
 PS Example 3; Fig 15; 102pp; English.

XX A cDNA clone (AA043437) codes for the heavy chain variable region
 CC (AA06212) of mouse monoclonal antibody (Mab) Br-3, and extends from
 CC the end of the oligo-dC tail to the JH3-CH1 junction. It was obtd.
 CC from a Br-3 hybridoma cDNA library by screening with a mouse IgG1
 CC C region probe. Mab Br-3 (IgG1) binds to an antigen that is
 CC expressed on the surface of human lung, breast, colon and ovary
 CC carcinomas, but not on most normal adult tissues. Light chain and
 CC heavy chain variable region (see also AA043434-43) sequences can be
 CC used with human constant region sequences to express mouse-human
 CC chimeric antibodies in transformed host cells. The antibodies have
 CC specificity to human tumor antigens and can be used for the
 CC treatment and diagnosis of human cancer.

XX SQ Sequence 497 BP; 141 A; 106 C; 118 G; 132 T; 0 other;

Query Match 70.7%; Score 293.6; DB 18; Length 497;
 Best Local Similarity 92.8%; Pred. No. 2.3e-78;
 Matches 308; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 52 TTTTATTTTATTTGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 111
 DB 92 TATTCATAGTTTCTCTCTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 151
 QY 112 GAGGCTTGTCGAACCTGGAGATCCATGAACCTCTCTGTGTAGCTCTGGATTTACTT 171
 DB 152 GAGGCTTGTCGAACCTGGAGATCCATGAACCTCTCTGTGTGTGTCTGGATTCACCT 211
 QY 172 TCAGTGGCTACTGGATGTCTTTGGTCCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGTG 231
 DB 212 TCAGTAACTATTGGATGAACCTGGTCCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGTG 271
 QY 232 CTGAATTTAGATTGAATCTGATTAATATGCAACACATTTATGCGGAGTCTGTGAAGGGA 291
 DB 272 CTGAATTTAGATTGAATCTGATTAATATGCAACACATTTATGCGGAGTCTGTGAAGGGA 331
 QY 292 AGTTCACCATCTCAAGAGATGATTCCAAAGTCTCTCTACCTGCAATGAACAGCTTAA 351
 DB 332 GGTTCACCATCTCAAGAGATGATTCCAAAGTCTCTCTACCTGCAATGAACAGCTTAA 391
 QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTACA 383
 DB 392 GAGCTGAAGACACTGGCATTATTACTGTACA 423

RESULT 8

AAQ85388
 ID AAQ85388 standard; cDNA; 480 BP.
 AC AAQ85388;
 XX

31-AUG-1995 (first entry)

MAB 4197X heavy chain variable region.

XX Immunotoxin; heavy chain; light chain; variable region; antibody;
 KW ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
 KW pH19; 4197X; monoclonal antibody; MAB; ds.
 XX

OS Synthetic.

XX Key Location/Qualifiers
 FH 1..480
 FT /*tag= a
 FT

XX WO9503828-A.

XX 09-FEB-1995.

XX 15-JUL-1994; 94WO-US07919.

XX 02-AUG-1993; 93US-0101329.

XX

PA (HOUS-) HOUSTON BIOTECHNOLOGY INC.

XX Gould RM, Kelleher PJ, Wallace RL, Wood MS;

XX WPI; 1995-082036/11.

DR P-PSDB; AAR70829.

XX New single chain immuno:toxin - binds specifically to epithelial
 PT cells, for inhibiting development of sec. cataracts after
 PT extra:capsular cataract extraction.

XX Disclosure; Fig.2; 68pp; English.

XX An immunotoxin (given in AAR70827) comprises the heavy (VH) and light
 CC chain (VL) variable regions of anti-lens epithelium IgG3 MAB 4197X
 CC linked to ricin-A. cDNAs encoding the VL and VH regions of 4197X
 CC (AAQ85387-88, respectively) were obtained from hybridoma mRNA,
 CC amplified by PCR, and engineered for inclusion in the immunotoxin
 CC construct (AAQ85386).

XX SQ Sequence 480 BP; 131 A; 105 C; 115 G; 129 T; 0 other;

Query Match 69.7%; Score 289.4; DB 16; Length 480;
 Best Local Similarity 92.1%; Pred. No. 4.2e-77;
 Matches 305; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 52 TTTTATTTTATTTGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 111
 DB 79 TATTCATAGTTTGTGTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 138
 QY 112 GAGGCTTGTCGAACCTGGAGATCCATGAACCTCTCTGTGTAGCCTCTGGATTTACTT 171
 DB 139 GAGGCTTGTCGAACCTGGAGATCCATGAACCTCTCTGTGTGTGTCTGCTCTGGATTCACCT 198
 QY 172 TCAGTGGCTACTGGATGTCTTGGTCCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGTG 231
 DB 199 TCAGTAACTCTGGATGAACCTGGTCCGCCAGTCTCCAGAGAAGGGCTTGAGTGGGTG 258
 QY 232 CTGAATTTAGATTGAATCTGATAATATGCAACACATTTATGCGGAGTCTGTGAAGGGA 291
 DB 259 CTGAATTTAGATTGAATCTGATAATATGCAACACATTTATGCGGAGTCTGTGAAGGGA 318
 QY 292 AGTTCACCATCTCAAGAGATGATTCCAAAGTCTCTACCTGCAATGAACAGCTTAA 351
 DB 319 GGTTCACCATCTCAAGAGATGATTCCAAAGTCTCTACCTGCAATGAACAGCTTAA 378
 QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
 DB 379 GAGCTGAAGACACTGGCATTATTACTGTAC 409

RESULT 9

AAQ12060
 ID AAQ12060 standard; DNA; 469 BP.
 XX

AC AAQ12060;

XX 15-AUG-1991 (first entry)

XX Sequence encoding heavy chain variable region of murine
 DE IC11 immunoglobulin.

XX Chimeric antibodies; immunoconjugates; HIV; AIDS; ss.

XX Mus musculus.

XX Key Location/Qualifiers
 FH 67..468
 FT /*tag= a

XX /product= mouse MAB IC11 H-chain variable region
 XX WO9107493-A.

AAV22331
ID AAV22331 standard; cDNA to mRNA; 357 BP.
XX
AC AAV22331;
XX
DT 06-JUL-1998 (first entry)
XX
DE Nucleic acid encoding synthetic branched mucin type glycolipid.
XX
KW Branched mucin type glycolipid; V region; heavy chain; antibody;
KW cancer treatment; diagnosis; ss.
XX
OS Synthetic.
XX
PN JP10084963-A.
XX
PD 07-APR-1998.
XX
PF 12-SEP-1996; 96JP-0241725.
XX
PR 12-SEP-1996; 96JP-0241725.
XX
PA (TOXJ) TOSOH CORP.
XX
WIPI; 1998-264850/24.
DR P-PSDB; AAW46958.
XX
XX
PT Recognising branched mucin type synthetic glycolipid - using gene
PT fragment of an antibody, useful in cancer treatment and diagnosis
PS
XX Claim 1; Pages 4-5; 6pp; Japanese.
XX
CC The present sequence encodes a branched mucin type synthetic
CC glycolipid. A gene fragment encoding the V region of the heavy
CC chain of an antibody recognising the protein encoded by the present
CC sequence is claimed. The antibody gene fragment is useful for the
CC development of cancer treatments and diagnosing agents.
XX
XX Sequence 357 BP; 99 A; 75 C; 93 G; 90 T; 0 other;
SQ
Query Match -65.5%; Score 272; DB 19; Length 357;
Best Local Similarity 94.9%; Pred. No. 6.4e-72;
Matches 281; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 87 GAAGTGAAGCTTGAGAGTCTGGAGAGGCTTGGTGCACCTGGAGATCCATGAACATC 146
DB 1 GAAGTGAAGCTTGAGAGTCTGGAGAGGCTTGGTGCACCTGGAGATCCATGAACATC 60
QY 147 TCCTGTGTAGCCCTCTGGATTACTTTTCAGTGGCTACTGGATGCTTGGTCCGCCAGTCT 206
DB 61 TCCTGTGTCCCTCTGGATTACTTTTCAGTGGCTACTGGATGCTTGGTCCGCCAGTCT 120
QY 207 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATAGATTGAAATCTGATTAATATGCAACA 266
DB 121 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATAGATTGAAATCTGATTAATATGCAACA 180
QY 267 CATTTGCGGAGTCTGTGAAGGGAAGTTACCATCTCAAGAGATGATTCGAAAGTCTGT 326
DB 181 CATTTGCGGAGTCTGTGAAGGGAAGTTACCATCTCAAGAGATGATTCGAAAGTCTGT 240
QY 327 CTCTACTGCAATGAACAGCTTAAAGAGCTGAAGACAGTGGATTTATTACTGTAC 382
DB 241 GTCTACTGCAATGAACAGCTTAAAGAGCTGAAGACAGTGGATTTATTACTGTAC 296
RESULT 12
ID AAC90472
XX AAC90472 standard; DNA; 856 BP.
AC AAC90472;
XX
XX
DT 13-MAR-2001 (first entry)
XX

DE Antibody 33F12 catalytic fragment nucleotide sequence.
XX
KW Antibody 33F12; ketone compound; antitumour; cytotoxic;
KW targeted drug delivery; ds.
XX
OS Unidentified.
XX
PN WO200071556-A1.
XX
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-US14366.
XX
PR 25-MAY-1999; 99US-0318661.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Barbas CF, Shabat D, Rader C, List B, Lerner RA;
XX
DR WIPI; 2001-061339/07.
DR P-PSDB; AAB50426.
XX
XX
PT New ketone compounds containing active agents useful as carriers for
PT e.g. antitumor agents, antibiotics or fluorescent molecules -
PS
XX Disclosure; Fig 10; 45pp; English.
XX
CC The present sequence may be used in the activation of new ketone prodrug
CC compounds containing active agents. The ketone derivatives are useful as
CC carriers for antitumour agents such as cytotoxic agents, where the
CC antitumour agent is a microtubule stabilising agent such as paclitaxel,
CC epothilone or its therapeutically active analogue or an anthracycline
CC antibiotic such as doxorubicin or its therapeutically active analogue.
CC The ketone derivatives are useful for targeted drug delivery.
CC The inactive molecules in the ketone compounds are converted to
CC active molecules by retro-Michael reaction. The antibody has
CC bifunctional activity and specifically immunoreacts with cell surface
CC antigen of a target cell. The active ingredients can be mixed
CC effectively with excipients as per desired amount along with the
CC buffering agent to enhance the effectiveness and activity of the
CC compound.
XX
SQ Sequence 856 BP; 195 A; 208 C; 228 G; 225 T; 0 other;
Query Match 65.4%; Score 271.6; DB 22; Length 856;
Best Local Similarity 92.3%; Pred. No. 1.2e-71;
Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 87 GAAGTGAAGCTTGAGAGTCTGGAGAGGCTTGGTGCACCTGGAGATCCATGAACATC 146
DB 450 GAGGTGATGCTGGTGGAGTCTGGAGAGGCTTGGTGCACCTGGAGATCCATGAACATC 519
QY 147 TCCTGTGTAGCCCTCTGGATTACTTTTCAGTGGCTTCTGGATGCTTGGTCCGCCAGTCT 206
DB 520 TCCTGTGTGGTGTCTGGATTAACTTTCAGTAGATTCTGGATGCTTGGTCCGCCAGTCT 579
QY 207 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATAGATTGAAATCTGATTAATATGCAACA 266
DB 580 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATAGATTGAAATCTGATTAATATGCAACA 639
QY 267 CATTTGCGGAGTCTGTGAAGGGAAGTTACCATCTCAAGAGATGATTCGAAAGTCTGT 326
DB 640 CATTTGCGGAGTCTGTGAAGGGAAGTTACCATCTCAAGAGATGATTCGAAAGTCTGT 699
QY 327 CTCTACTGCAATGAACAGCTTAAAGAGCTGAAGACAGTGGATTTATTACTGTACAGAT 386
DB 700 CTCTACTGCAATGAACAGCTTAAAGAGCTGAAGACAGTGGATTTATTACTGTACAGAT 759
QY 387 TTCATAGACT 396
DB 760 TATTTTACT 769

RESULT 13

AAQ85386
ID AAQ85386 standard; DNA: 1979 BP.
XX
AC AAQ85386;
XX
DT 31-AUG-1995 (first entry)
DE Anti-cataract immunotoxin in pHb19.
XX
KW Immunotoxin; heavy chain; light chain; variable region; antibody;
KW ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
KW pHb19; 4197X; monoclonal antibody; MAb; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 115..1779
FT /*tag= a
FT sig_peptide 115..195
FT /*tag= b
FT /note= "phoA signal sequence"
FT mat_peptide 196..1776
FT /*tag= c
XX
PN WO9503828-A.
XX
PD 09-FEB-1995.
XX
PF 15-JUL-1994; 94WO-US07919.
XX
PR 02-AUG-1993; 93US-0101329.
XX
PA (HOUS-) HOUSTON BIOTECHNOLOGY INC.
XX
PI Gould RM, Kelleher PJ, Wallace TL, Wood MS;
XX
XX WPI: 1995-082036/11.
DR P-PSDB; AAR70827.
XX
XX New single chain immuno:toxin - binds specifically to epithelial
XX cells, for inhibiting development of sec. cataracts after
XX extra:capsular cataract extraction.
XX
XX Disclosure; Fig.4; 68pp; English.
XX
CC The immunotoxin given in AAR70827 comprises the heavy and light chain
CC variable regions of anti-lens epithelium IgG3 MAb 4197X linked to
CC ricin-A and a hexa-histidine tag. The DNA construct encoding the
CC immunotoxin was expressed from pHb19 in E. coli.
XX
SQ Sequence 1979 BP; 558 A; 426 C; 459 G; 536 T; 0 other;
XX
Query Match 65.08; Score 269.8; DB 16; Length 1979;
Best Local Similarity 94.3%; Pred. No. 5.6e-71;
Matches 280; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 86 TGAAGTGAAGCTTGAGGAGCTGGAGGAGCTGGTGCACCTGGAGATCCATGAACACT 145
DB 198 TGAAGTGAAGCTTGAGGAGCTGGAGGAGCTGGTGCACCTGGAGATCCATGAACACT 257
QY 146 CTCCTGTGTAGCCTCTGATTACTTTCAGTGGCTACTGGATGCTTGGTCCGCCAGTC 205
DB 258 CTCCTGTGTGCTCTGGATTCACCTTCAGTAACTTCGTGAATCTGAGTGGTCCGCCAGTC 317
QY 206 TCAGAGAGGGGCTTGAGTGGTGGTGGTGAATAGATTCGAATCTGATTAATATCAAC 265
DB 318 TCAGAGAGGGGCTTGAGTGGTGGTGGTGAATAGATTCGAATCTGATTAATATCAAC 377
QY 266 ACATTATGCGGAGCTGTGAAGGGAAGTTCCACCATCTCAAGAGATGATTCCAAAAGTCG 325
DB 378 ACATTATGCGGAGCTGTGAAGGGAAGTTCCACCATCTCAAGAGATGATTCCAAAAGTAG 437

QY 326 TCTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGGAGTTTATTACTGTAC 382
DB 438 TGTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGGCATTATTACTGTAC 494

RESULT 14

AAQ62750
ID AAQ62750 standard; cDNA: 403 BP.
XX
AC AAQ62750;
XX
DT 24-JAN-1995 (first entry)
DE Murine BrE-3 immunoglobulin heavy chain variable domain cDNA.
XX
KW Immunoglobulin variable domain; primer; polymerase chain reaction;
KW chimeric antibody; human milk fat globule; BrE-3 VH-chain; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1..402
FT /*tag= a
FT /note= "BrE-3 VH chain (no termination codon)"
FT mat_peptide 58..402
FT /*tag= b
FT /product= heavy_chain_V-region
XX
PN WO9411508-A.
XX
PD 26-MAY-1994.
XX
PF 15-NOV-1993; 93WO-US11316.
XX
PR 13-NOV-1992; 92US-0977706.
PR 13-NOV-1992; 92US-0977707.
PR 28-SEP-1993; 93US-0128015.
XX
XX (CANC-) CANCER RES FUND CONTRA COSTA.
XX
XX WPI: 1994-183509/22.
DR P-PSDB; AAR52771.
XX
XX Chimeric human-murine polypeptide(s) specific for human mammary
XX fat globule antigen - for imaging, diagnosing and treating
XX neoplasia, with less undesirable immunogenic response
XX
XX Example 10; Page 32; 54pp; English.
XX
CC Primers JO2, JO3, JO4, JO14 and VHLBACK (AAQ62740-Q62744) were all
CC used to prepare cDNAs that encode the BrE-3 mouse Ig variable
CC domains. The amplified V-regions lacked constant regions so as to
CC produce less immunogenic polypeptides. A hybrid polypeptide was
CC prepared using human constant regions with the murine V regions.
CC The chimeric polypeptide retained the binding affinity of BrE-3
CC for human milk fat globule.
XX
SQ Sequence 403 BP; 105 A; 73 C; 113 G; 112 T; 0 other;
XX
Query Match 64.9%; Score 269.4; DB 15; Length 403;
Best Local Similarity 85.3%; Pred. No. 4.1e-71;
Matches 313; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

QY 52 TTTTATTTATTTCTTTTAAAGGGGTCCAGAGTGAAGTGAAGCTTGAGAGTCTGGAG 111
DB 23 TCTTCATAGTTTTCTCTCTTAAAGGTGTCCAGAGTGAAGCTTGAGAGTCTGGAG 82
QY 112 GAGGCTGTGCAACCTGGAGGATCCATCACTCTCTGTAGCCTCTGGATTACTT 171
DB 83 GAGGCTGTGCAACCTGGAGGATCCATCACTCTCTGTAGCCTCTGGATTACTT 142
QY 172 TCAGTGGCTACTGGATGCTCTTGGTCCGCCAGTCTCCAGAGAGGGCTTGAGTGGTGTG 231

```
Db 143 TTAGTGATGCTGGTGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTG 202
Qy 232 CTGAATAGATTGAATCTGATATATGCAACACATATTCGGGAGTCTGTGAAGGGA 291
Db 203 CTGAATAGATTGAATCTGATATATGCAACACATATTCGGGAGTCTGTGAAGGGA 262
Qy 292 AGTTCACCATCTCAAGAGATGATTCACAAAGTCGTCTACCTGCAAAATGAACAGCTTAA 351
Db 263 GGTTCACCATCTCAAGAGATGATTCACAAAGTCGTCTACCTGCAAAATGAACAGCTTAA 322
Qy 352 GAGCTGAAGACAGTGGGTTTATTACTGTAC---AGATTTCATAGACTGGGGCCAAAGGGA 408
Db 323 GAGCTGAAGACAGTGGGTTTATTACTGTAC---AGATTTCATAGACTGGGGCCAAAGGGA 382
Qy 409 CACTAGT 415
Db 383 CTCTGGT 389

RESULT 15
AAQ62775
ID AAQ62775 standard; cDNA; 403 BP.
XX AC
XX AAQ62775;
XX DT
XX 24-JAN-1995 (first entry)
XX DE Murine BrE-3 immunoglobulin heavy chain variable domain cDNA.
XX KW Immunoglobulin variable domain; primer; polymerase chain reaction;
XX KW chimeric antibody; human milk fat globule; BrE-3 VH-chain; ss.
XX OS Mus musculus.
XX FH
XX Key Location/Qualifiers
XX FT 1..402
XX CDS /tag= a
XX FT /note= "BrE-3 VH chain (no termination codon)"
XX FT mat_peptide 58..402
XX FT /*tag= b
XX FT /product= heavy_chain_V-region
XX FN
XX WO9411509-A.
XX PD
XX 26-MAY-1994.
XX PF
XX 16-NOV-1993; 93WO-US11445.
XX PR
XX 16-NOV-1992; 92US-0977696.
XX PR 30-SEP-1993; 93US-0129930.
XX PR 08-OCT-1993; 93US-0134346.
XX XX
XX (CANC-) CANCER RES FUND CONTRA COSTA.
XX PI
XX Ceriani RL, Do Couto FJR, Padlan EA, Peterson JA;
XX WPT; 1994-183510/22.
XX DR
XX New analogue peptide(s) comprising antibody variable regions -
XX PT used to develop prods. for use in the detection, diagnosis,
XX PT therapy and prevention of neoplasms
XX PS
XX Example 11; Page 48; 109pp; English.
XX CC
XX Primers J02, J03, J04, J014 and VHLBACK (AAQ62765-Q62769) were all
XX CC used to prepare cDNAs that encode the BrE-3 mouse Ig variable
XX CC domains. The amplified V-regions lacked constant regions so as to
XX CC produce less immunogenic polypeptides. A hybrid polypeptide was
XX CC prepared using human constant regions with the murine V regions.
XX CC The chimeric polypeptide retained the binding affinity of BrE-3
XX CC for human milk fat globule.
XX SQ
Sequence 403 BP; 105 A; 73 C; 113 G; 112 T; 0 other;
```

```
Query Match 64.9%; Score 269.4; DB 15; Length 403;
Best Local Similarity 85.3%; Pred. No. 4.1e-71;
Matches 313; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
Qy 52 TTTTATTTTATTTCTTTTAAAAAGGGTCCAGAGTGAAGCTTGAAGAGTCTGAG 111
Db 23 TCTTCATAGATTTTCTCTTAAAGGTGTCAGAGTGAAGCTTGAAGAGTCTGAG 82
Qy 112 GAGCTTGGTGGCAACCTGGAGGATCCATGAAACTCTCTCTGTGTAGCCCTCTGGATTTACTT 171
Db 83 GAGCTTGGTGGCAACCTGGAGGATCCATGAAACTCTCTCTGTGTGTCTCTTCTGGATTCAC 142
Qy 172 TCAGTGGTACTGATGTCTCTGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTG 231
Db 143 TTAGTGATGCTGGTGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTG 202
Qy 232 CTGAATAGATTGAATCTGATATATGCAACACATATTCGGGAGTCTGTGAAGGGA 291
Db 203 CTGAATAGATTGAATCTGATATATGCAACACATATTCGGGAGTCTGTGAAGGGA 262
Qy 292 AGTTCACCATCTCAAGAGATGATTCACAAAGTCGTCTCTACCTGCAAAATGAACAGCTTAA 351
Db 263 GGTTCACCATCTCAAGAGATGATTCACAAAGTCGTCTCTACCTGCAAAATGAACAGCTTAA 322
Qy 352 GAGCTGAAGACAGTGGGTTTATTACTGTAC---AGATTTCATAGACTGGGGCCAAAGGGA 408
Db 323 GAGCTGAAGACAGTGGGTTTATTACTGTAC---AGATTTCATAGACTGGGGCCAAAGGGA 382
Qy 409 CACTAGT 415
Db 383 CTCTGGT 389
```

Search completed: April 26, 2003, 05:05:43
Job time : 86.4911 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 07:27:07 ; Search time 40.1085 seconds
(without alignments)
11258.801 Million cell updates/sec

Title: US-09-674-716B-1

Perfect score: 415

Sequence: 1 agccttaccattactcagc.....tggggccaaggacactagt 415

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 709820 seqs, 544064369 residues

Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	310.4	74.8	453	10	US-09-564-329A-14
2	310.4	74.8	453	10	US-09-855-153-14
3	310.4	74.8	453	10	US-09-854-811-14
4	310.4	74.8	453	10	US-09-934-773-14
5	310.4	74.8	453	10	US-09-963-620-14
6	271.6	65.4	856	10	US-09-883-758-3
c 7	271.6	65.4	856	10	US-09-883-758-6
c 8	263.6	63.5	899	10	US-09-883-758-1
c 9	263.6	63.5	899	10	US-09-883-758-5
10	256	61.7	357	9	US-10-043-432-4
11	256	61.7	357	10	US-09-756-301A-4
12	256	61.7	357	10	US-09-927-703-4
13	256	61.7	357	10	US-09-766-535A-4
14	256	61.7	357	10	US-09-756-161A-4
15	256	61.7	357	12	US-10-010-229-4
16	256	61.7	357	12	US-10-043-450-4
17	256	61.7	357	12	US-10-044-534-4
18	204	49.2	443	10	US-09-840-459-96
c 19	204	49.2	443	10	US-09-840-459-99
					Sequence 14, Appl
					Sequence 14, Appl
					Sequence 14, Appl
					Sequence 14, Appl
					Sequence 14, Appl
					Sequence 3, Appl
					Sequence 6, Appl
					Sequence 1, Appl
					Sequence 5, Appl
					Sequence 4, Appl
					Sequence 4, Appl
					Sequence 4, Appl
					Sequence 4, Appl
					Sequence 96, Appl
					Sequence 99, Appl

20	198.4	47.8	466	10	US-09-881-823-15	Sequence 15, Appl
21	196.2	47.3	406	9	US-10-046-935-2168	Sequence 2168, Ap
22	196.2	47.3	406	9	US-09-878-178-2168	Sequence 2168, Ap
23	196.2	47.3	406	9	US-10-146-502-2168	Sequence 2168, Ap
24	194.8	46.9	424	10	US-09-730-857-28	Sequence 28, Appl
25	193.2	46.6	364	7	US-08-779-784-14	Sequence 14, Appl
26	191.6	46.2	423	7	US-08-779-784-3	Sequence 3, Appl
27	189.8	45.7	442	10	US-09-905-243-42	Sequence 42, Appl
28	189	45.5	545	10	US-09-925-301-16	Sequence 16, Appl
29	187.4	45.2	424	10	US-09-730-857-62	Sequence 62, Appl
30	186.8	45.0	369	10	US-09-893-615-86	Sequence 86, Appl
31	186.8	45.0	1437	9	US-10-124-905-7	Sequence 7, Appl
32	186.8	45.0	1437	9	US-09-948-429B-7	Sequence 7, Appl
33	186.8	45.0	1437	9	US-10-073-138-4	Sequence 4, Appl
34	185.8	44.8	424	10	US-09-730-857-50	Sequence 50, Appl
35	185.8	44.8	424	10	US-09-730-857-54	Sequence 54, Appl
36	185.8	44.8	424	10	US-09-730-857-64	Sequence 64, Appl
37	185.6	44.7	357	10	US-09-840-459-97	Sequence 97, Appl
c 38	185.6	44.7	357	10	US-09-840-459-103	Sequence 103, Appl
39	184.2	44.4	424	10	US-09-730-857-48	Sequence 48, Appl
40	184.2	44.4	424	10	US-09-730-857-58	Sequence 58, Appl
41	184.2	44.4	424	10	US-09-730-857-58	Sequence 58, Appl
42	184	44.3	690	9	US-10-125-237-73	Sequence 73, Appl
43	184	44.3	690	9	US-10-105-891-73	Sequence 73, Appl
44	183.6	44.2	630	9	US-10-040-244-14	Sequence 14, Appl
45	183.6	44.2	630	10	US-09-844-684-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-09-564-329A-14
; Sequence 14, Application US/09564329A
; Patent No. US20010055751A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSQA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/564,329A
; CURRENT FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-09-564-329A-14

RESULT 4
 US-09-934-773-14
 ; Sequence 14, Application US/09934773
 ; Patent No. US20020136689A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiter, Robert E.
 ; APPLICANT: Witte, Owen N.
 ; APPLICANT: Saffran, Douglas C.
 ; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
 ; FILE REFERENCE: 30435.54US14
 ; CURRENT APPLICATION NUMBER: US/09/934,773
 ; CURRENT FILING DATE: 2001-08-21
 ; PRIOR APPLICATION NUMBER: 09/564,329
 ; PRIOR FILING DATE: 2000-05-03
 ; PRIOR APPLICATION NUMBER: 09/359,326
 ; PRIOR FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: 08/814,279
 ; PRIOR FILING DATE: 1997-03-10
 ; PRIOR APPLICATION NUMBER: 60/071,141
 ; PRIOR FILING DATE: 1998-01-12
 ; PRIOR APPLICATION NUMBER: 60/074,675
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: 60/113,230
 ; PRIOR FILING DATE: 1998-12-21
 ; PRIOR APPLICATION NUMBER: 60/120,536
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 60/124,658
 ; PRIOR FILING DATE: 1999-03-16
 ; PRIOR APPLICATION NUMBER: 09/038,261
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 09/203,939
 ; PRIOR FILING DATE: 1998-12-02
 ; PRIOR APPLICATION NUMBER: 09/251,835
 ; PRIOR FILING DATE: 1999-02-17
 ; PRIOR APPLICATION NUMBER: 09/308,503
 ; PRIOR FILING DATE: 1999-05-25
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn ver. 2.0
 ; SEQ ID NO 14
 ; LENGTH: 453
 ; TYPE: DNA
 ; ORGANISM: SCID Mice
 US-09-934-773-14

Qy	275	GGATCTGTGTAAGGGGAGTTCACCATCTCAGACGATGATTCACCAAGTCGTCTTACCT	334
Db	246	GGATCTGTGTAAGGGGAAATTCACCATCTCAGACGATGATTCGAAGTCGTCTTACCT	305
Qy	335	GCAATGAACAGCTTAAAGAGCTGAAGACAGCTGGAGTTTATTACTGTACAGAT	386
Db	306	GCAATGAACAACTTAAAGAGCTGAAGACAGCTGGAATTTATTACTGTACAGAT	357

```

US-09-963-620-14
; Sequence 14, Application US/09963620
; Patent No. US20020141941A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.540S14
; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 453
; TYPE: DNA
; ORGANISM: SCID Mice
US-09-963-620-14

```

Query Match	74.8%;	Score 310.4;	DB 10;	Length 453;
Best Local Similarity	92.6%;	Pred. No. 1.4e-87;		
Matches 326;	Conservative 0;	Mismatches 26;	Indels 0;	Gaps 0;
QY	35	CATGGATTTGGCGTCATTTTTTTTTTATTCCTCTTTTAAAGGGGTCAGAGTGAAGTGA	94	
Db	6	CTTCGGTTGAGCTGGTTTTTATTTATTTCTTTTAAAGGGGTCGGAGTCAAGTGAG	65	
QY	95	GCTTGAGGAGTCTGGAGGAGGCTTGGTGCACCTGGAGATCCATGAAACTCTCCTGTGT	154	
Db	66	GCTTGAGGAGTCTGGAGGAGGCTGGGTGCAACCTGGAGATCCATGAAACTCTCCTGTGT	125	
QY	155	AGCCTCTGATTTACCTTCAGTGGCTTACGTGATGCTCTTGGTCCGCGACTCTCCAGAGAA	214	
Db	126	AGCCTCTGATTTACCTTCAGTATTTTCTTGGATGACTTGGGTCCGCCACTCTCCAGAGAA	185	
QY	215	GGGGCTTGAGTGGGGTTGCTCAAAATTAGATTGAATCTGATAATTATGCAACACATTATGC	274	
Db	186	GGGGCTTGAGTGGGTGCTGAAATTCGATTTGAGATCTGAAATTTATGCAACACATTATGC	245	

QY 275 GGAGTCTGTGAAGGGAAGTCCACCATCTCAAGAGATGATTCCAAAGTGGTCTCTACT 334
|||||
Db 246 GGAGTCTGTGAAGGGAAGTCCACCATCTCAAGAGATGATTCCAAAGTGGTCTCTACT 305
|||||
QY 335 GCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTCTTATTACTGTACAGAT 386
|||||
Db 306 GCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTCTTATTACTGTACAGAT 357
|||||

RESULT 6

US-09-883-758-3
; Sequence 3, Application US/09883758
; Patent No. US20020058804A1
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/883,758
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment.
; NAME/KEY: CDS
; LOCATION: (1)..(855)
US-09-883-758-3

Query Match 65.4%; Score 271.6; DB 10; Length 856;
Best Local Similarity 92.3%; Pred. No. 3e-75;
Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAAGTCT 146
|||||
Db 460 GAGGTGCTGTGGTGGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAAGTCT 519
|||||
QY 147 TCCTGTGTAGCTCTGGATTTACTTTTCAGTGGCTTACTGGATGCTTGGGTCGCCAGTCT 206
|||||
Db 520 TCCTGTGTGGTCTGGATTTAACTTCAAGTATCTTGGATGCTTGGGTCGCCAGTCT 579
|||||
QY 207 CCAGAGAAGGGGCTTGAGTGGTGTCTGAAATAGATTGAAATCTGATAATTATGCAACA 266
|||||
Db 580 CCAGAGAAGGGGCTTGAGTGGTGTCTGAAATAGATTGAAATCTGATAATTATGCAACA 639
|||||
QY 267 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTGT 326
|||||
Db 640 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTGT 699
|||||
QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTTTATTACTGTACAGAT 386
|||||
Db 700 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTTTATTACTGTAAATATC 759
|||||

RESULT 7

US-09-883-758-6/c
; Sequence 6, Application US/09883758
; Patent No. US20020058804A1
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.

; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/883,758
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment.
US-09-883-758-6

Query Match 65.4%; Score 271.6; DB 10; Length 856;
Best Local Similarity 92.3%; Pred. No. 3e-75;
Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAAGTCT 146
|||||
Db 397 GAGGTGATGCTGGTGGAGTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAAGTCT 338
|||||
QY 147 TCCTGTGTAGCTCTGGATTTACTTTTCAGTGGCTTACTGGATGCTTGGGTCGCCAGTCT 206
|||||
Db 337 TCCTGTGTGGTCTGTGGATTTAACTTCAAGTATCTTGGATGCTTGGGTCGCCAGTCT 278
|||||
QY 207 CCAGAGAAGGGGCTTGAGTGGTGTCTGAAATAGATTGAAATCTGATAATTATGCAACA 266
|||||
Db 277 CCAGAGAAGGGGCTTGAGTGGTGTCTGAAATAGATTGAAATCTGATAATTATGCAACA 218
|||||
QY 267 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTGT 326
|||||
Db 217 CATTATCGGAGTCTGTGAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCTGT 158
|||||
QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTTTATTACTGTACAGAT 386
|||||
Db 157 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTTTATTACTGTAAATATC 98
|||||

QY 387 TTCATAGACT 396
| | | | |
Db 97 TATTTTACT 88
| | | | |

RESULT 8

US-09-883-758-1
; Sequence 1, Application US/09883758
; Patent No. US20020058804A1
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/883,758
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 899
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:

QY 87 GAAGTGAAGCTTGAGGAGCTCTGGAGGAGCTTGGTCAACCTGGAGATCCATGAACATC 146
Db 1 GAAGTGAAGCTTGAGGAGCTCTGGAGGAGCTTGGTCAACCTGGAGATCCATGAACATC 60
QY 147 TCCTGTGTAGCTCTGGATTACTTTTCAGTGGCTTACTGGATGCTTGGGTCGCCAGTCT 206
Db 61 TCCTGTGTAGCTCTGGATTACTTTTCAGTGGCTTACTGGATGCTTGGGTCGCCAGTCT 120
QY 207 CCAGAGAAGGGCTTGAGTGGGTTGCTGAAATAGATTGAAATCTGATAATATGCAACA 266
Db 121 CCAGAGAAGGGCTTGAGTGGGTTGCTGAAATAGATTGAAATCTGATAATATGCAACA 180
QY 267 CATTATCGGAGCTCTGTAAGGGAAGTTCACCATCTCAAGAGATGATCCAAAGTCGT 326
Db 181 CATTATCGGAGCTCTGTAAGGGAAGTTCACCATCTCAAGAGATGATCCAAAGTCGT 240
QY 327 CTCACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
Db 241 GTCACCTGCAAAATGACCGACTTAAGAACTGAAGACACTGGCGTTTATTACTGTTC 296

RESULT 13

US-09-766-535A-4
; Sequence 4, Application US/09766535A
; Patent No. US20020106372A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-010
; CURRENT APPLICATION NUMBER: US/09766,535A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Mus Balb/c
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(357)
US-09-766-535A-4

Query Match 61.7%; Score 256; DB 10; Length 357;
Best Local Similarity 91.6%; Pred. No. 1.6e-70;

Matches 271; Conservative 0; Mismatches 25; Indels 0; Gaps 0:
QY 87 GAAGTGAAGCTTGAGGAGCTCTGGAGGAGCTTGGTCAACCTGGAGATCCATGAACATC 146
Db 1 GAAGTGAAGCTTGAGGAGCTCTGGAGGAGCTTGGTCAACCTGGAGATCCATGAACATC 60
QY 147 TCCTGTGTAGCTCTGGATTACTTTTCAGTGGCTTACTGGATGCTTGGGTCGCCAGTCT 206
Db 61 TCCTGTGTAGCTCTGGATTACTTTTCAGTGGCTTACTGGATGCTTGGGTCGCCAGTCT 120
QY 207 CCAGAGAAGGGCTTGAGTGGGTTGCTGAAATAGATTGAAATCTGATAATATGCAACA 266
Db 121 CCAGAGAAGGGCTTGAGTGGGTTGCTGAAATAGATTGAAATCTGATAATATGCAACA 180
QY 267 CATTATCGGAGCTCTGTAAGGGAAGTTCACCATCTCAAGAGATGATCCAAAGTCGT 326
Db 181 CATTATCGGAGCTCTGTAAGGGAAGTTCACCATCTCAAGAGATGATCCAAAGTCGT 240
QY 327 CTCACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
Db 241 GTCACCTGCAAAATGACCGACTTAAGAACTGAAGACACTGGCGTTTATTACTGTTC 296

RESULT 14

US-09-756-161A-4
; Sequence 4, Application US/09756161A
; Patent No. US2002013207A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Grayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-007
; CURRENT APPLICATION NUMBER: US/09756,161A
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; PRIOR FILING DATE: 1991-03-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Mus Balb/c
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(357)
US-09-756-161A-4

Query Match 61.7%; Score 256; DB 10; Length 357;

Best Local Similarity 91.6%; Pred. No. 1.6e-70;
Matches 271; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

```
QY 87 GAAGTGAAGCTTGGAGAGTCTGGAGAGGCTTGGTGCACACCTGGAGGATCCATGAAACTC 146
Db 1 GAAGTGAAGCTTGGAGAGTCTGGAGAGGCTTGGTGCACACCTGGAGGATCCATGAAACTC 60
QY 147 TCCTGTGTAGCCTCTGGATTTACTTTTCAGTGGCTACTGGATGCTCTGGTCCGCCAGTCT 206
Db 61 TCCTGTGTGTCTGGATTTACTTTTCAGTAACTGATGAACTGATGAACTGATGAACTGAT 120
QY 207 CCAGAGAAGGGCTTGGTGGTCTGCTGAAATAGATTGAAATCTGATGAAATCTGATGAA 266
Db 121 CCAGAGAAGGGCTTGGTGGTCTGCTGAAATAGATTGAAATCTGATGAAATCTGATGAA 180
QY 267 CATTATCGGAGTCTGTGAAAGGGAGTTCCACCATCTCAAGAGATGATTCACAAAGTCT 326
Db 181 CATTATCGGAGTCTGTGAAAGGGAGTTCCACCATCTCAAGAGATGATTCACAAAGTCT 240
QY 327 CTCTACCTGCAATGAACAGCTTAAAGCTGAAGAGCTGAAGAGCTGGAGTTTACTGTAC 382
Db 241 GTCTACCTGCAATGAACAGCTTAAAGCTGAAGAGCTGAAGAGCTGGAGTTTACTGTTC 296
```

RESULT 15

US-10-010-229-4

; Sequence 4, Application US/10010229.

; Patent No. US20020114805A1

; GENERAL INFORMATION:

; APPLICANT: Le, Junming

; APPLICANT: Vilcek, Jan

; APPLICANT: Daddona, Peter

; APPLICANT: Grayeb, John

; APPLICANT: Knight, David M.

; APPLICANT: Siegel, Scott

; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of

; FILE REFERENCE: Human Tumor Necrosis Factor

; CURRENT APPLICATION NUMBER: US/10/010,229

; PRIOR FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: US/09/927,703

; PRIOR FILING DATE: 2001-08-10

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 357

; TYPE: DNA

; ORGANISM: Mus Balb/c

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(357)

US-10-010-229-4

Query Match

Best Local Similarity 61.7%; Score 256; DB 12; Length 357;

Matches 271; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

```
QY 87 GAAGTGAAGCTTGGAGAGTCTGGAGAGGCTTGGTGCACACCTGGAGGATCCATGAAACTC 146
Db 1 GAAGTGAAGCTTGGAGAGTCTGGAGAGGCTTGGTGCACACCTGGAGGATCCATGAAACTC 60
QY 147 TCCTGTGTAGCCTCTGGATTTACTTTTCAGTGGCTACTGGATGCTTGGTCCGCCAGTCT 206
Db 61 TCCTGTGTGTCTGGATTTACTTTTCAGTAACTGATGAACTGATGAACTGATGAACTGAT 120
QY 207 CCAGAGAAGGGCTTGGTGGTCTGCTGAAATAGATTGAAATCTGATGAAATCTGATGAA 266
Db 121 CCAGAGAAGGGCTTGGTGGTCTGCTGAAATAGATTGAAATCTGATGAAATCTGATGAA 180
QY 267 CATTATCGGAGTCTGTGAAAGGGAGTTCCACCATCTCAAGAGATGATTCACAAAGTCT 326
Db 181 CATTATCGGAGTCTGTGAAAGGGAGTTCCACCATCTCAAGAGATGATTCACAAAGTCT 240
```

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	271.6	65.4	856	4	US-09-318-661-3	Sequence 3, Appli
2	271.6	65.4	856	4	US-09-318-661-6	Sequence 6, Appli
c	269.4	64.9	403	1	US-07-977-696C-12	Sequence 12, Appli
3	269.4	64.9	403	1	US-08-129-930B-12	Sequence 12, Appli
4	269.4	64.9	403	1	US-08-976-288A-12	Sequence 12, Appli
5	269.4	64.9	403	1	US-08-976-288A-12	Sequence 12, Appli
6	267.8	64.4	360	3	US-08-767-128-27	Sequence 27, Appli
7	267.2	64.4	366	3	US-08-483-749A-1	Sequence 1, Appli
8	263.6	63.5	899	4	US-09-318-661-1	Sequence 1, Appli
9	263.6	63.5	899	4	US-09-318-661-5	Sequence 5, Appli
c	263.6	63.5	899	4	US-07-977-696C-65	Sequence 65, Appli
10	263.6	63.4	403	1	US-07-977-696C-65	Sequence 65, Appli
11	263.6	63.4	403	1	US-08-129-930B-65	Sequence 65, Appli
12	263.6	63.4	403	1	US-08-976-288A-65	Sequence 65, Appli
13	259.6	62.4	342	3	US-08-483-749A-9	Sequence 9, Appli
14	256.6	61.8	357	3	US-08-767-128-25	Sequence 25, Appli
15	256.6	61.7	357	3	US-08-192-102-4	Sequence 4, Appli
16	256.6	61.7	357	1	US-08-324-799-4	Sequence 4, Appli
17	256.6	61.7	357	2	US-08-192-861A-4	Sequence 4, Appli
18	256.6	61.7	357	4	US-09-133-119-4	Sequence 4, Appli
19	256.6	61.7	357	4	US-08-192-099A-4	Sequence 4, Appli
20	244.4	58.9	345	1	US-08-468-661-2	Sequence 2, Appli
21	244.4	58.9	345	1	US-08-468-661-2	Sequence 2, Appli
22	244.4	58.9	345	1	US-08-468-272A-2	Sequence 2, Appli
23	244.4	58.9	345	1	US-08-471-771-2	Sequence 2, Appli
24	244.4	58.9	345	3	US-08-471-771-2	Sequence 2, Appli
25	229.4	55.3	738	2	US-09-130-783-2	Sequence 2, Appli
26	229.4	55.3	738	2	US-08-224-591-13	Sequence 13, Appli
27	229.4	55.3	738	2	US-08-392-338A-22	Sequence 22, Appli
28	229.4	55.3	738	2	US-08-926-789-13	Sequence 13, Appli

QY 387 TTCATAGACT 396
| | | | |
Db 760 TATTTTACT 769

RESULT 2

US-09-318-661-6/c
; Sequence 6, Application US/09318661
; Patent No. 6268488
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/318,661
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 856
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment.
US-09-318-661-6

Query Match 65.4%; Score 271.6; DB 4; Length 856;
Best Local Similarity 92.3%; Pred. No. 1.7e-72;
Matches 286; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 87 GAAGTGAAGCTTGGAGGCTCTGGAGGAGCTGGTCAACCTGGAGGATCCATGAACCTC 146
| | | | |
Db 397 GAGGTGATGCTGGTGGAGCTGGAGGAGGCTGGTCAACCTGGAGGATCCATGAACCTC 338
QY 147 TCCTGTGTAGCTTGAATTTACTTTTCAGTGGCTACTGGATGCTTTGGGGTCCGCCAGTCT 206
| | | | |
Db 337 TCCTGTGTGTCTGGATTAACCTTCAGTAGATTCCTGGATGCTTTGGGTCCGCCAGTCT 278
QY 207 CCAGAGAAGGGCTTGTAGTGGTGTCTGAATAGATTGAATCTGATAATTTATGAACA 266
| | | | |
Db 277 CCAGAGAAGGGCTTGTAGTGGTGTCTGAATAGATTGAATCTGATAATTTATGAACA 218
QY 267 CATTTATCGGAGTCTGTGAAGGGAAGTTCCACCATCTCAAGAGATGATTCCTCAAGTTCGT 326
| | | | |
Db 217 CATTTATCGGAGTCTGTGAAGGGAAGTTCCACCATCTCAAGAGATGATTCCTCAAGTTCGT 158
QY 327 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTTTTACTCTACAGAT 386
| | | | |
Db 157 CTCTACCTGCAATGAACAGCTTAAGAGCTGAAGAGCTGAAGAGCTTTTACTCTGAATTC 98
QY 387 TTCATAGACT 396
| | | | |
Db 97 TATTTTACT 88

RESULT 3

US-07-977-696C-12
; Sequence 12, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
; TITLE OF INVENTION: and Therapeutic Methods.
; NUMBER OF SEQUENCES: 81

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,696C
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6688
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-977-696C-12

Query Match 64.9%; Score 269.4; DB 1; Length 403;
Best Local Similarity 85.3%; Pred. No. 6.2e-72;
Matches 313; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
QY 52 TTTTCTTTTATTCTTTTAAAGGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 111
| | | | |
Db 23 TCTTCATAGTCTTTCTTTAAAGGTGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 82
QY 112 GAGGCTTGTGCAACCTGGAGGATCCATGAACCTCTCTGTGTAGCCCTCTGGATTACTT 171
| | | | |
Db 83 GAGGCTTGTGCAACCTGGAGGATCCATGAACCTCTCTGTGTAGCCCTCTGGATTACTT 142
QY 172 TCAGTGGCTTACTGGATGCTTTGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGTGG 231
| | | | |
Db 143 TTAGTGATGCTTGGATGCTGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGTGG 202
QY 232 CTGAATTTAGATTGAATCTGATAATTATGCAACACATTTATGCGGAGTCTGTGAAGGGA 291
| | | | |
Db 203 CTGAATTTAGAACCAAGCCCAATATATGCAACATATATGATGATGATGATGATGATGAT 262
QY 292 AGTTCCACCATCTCAAGAGATGATTCCTCAAGAGTCTCTACCTGCAATGAACAGCTTAA 351
| | | | |
Db 263 GGTTCACCATCTCAAGAGATGATTCCTCAAGAGTCTCTACCTGCAATGAATGATGATGAT 322
QY 352 GAGCTGAAGACAGTGGAGTCTTTTACTGTAC---AGATTTCATAGACTGGGCCCAAGGGA 408
| | | | |
Db 323 GAGCTGAAGACACTGGCCTTTTATTACTGTCTGGGGAGCTTTGCTTAACCTGGGCCAGGGA 382
QY 409 CACTAGT 415
| | | | |
Db 383 CTCCTGGT 389

RESULT 4

US-08-129-930B-12
; Sequence 12, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.

APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: V. ANZEL & ASSOC.
STREET: 2055 No. 5804187th Broadway, Suite 201
CITY: Walnut Creek
STATE: California
COUNTRY: USA
ZIP: 94596
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,930B
FILING DATE: September 30, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Anzel Ph.D., Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: CRFCC-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 521-1333
TELEFAX: (510) 521-3541
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-129-930B-12

Query Match 64.9%; Score 269.4; DB 1; Length 403;
Best Local Similarity 85.3%; Pred. No. 6.2e-72;
Matches 313; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
Qy 52 TTTTATTTATTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGTTCGAGAGTCTGGAG 111
Db 23 TCTCATAGTTTCTTTCTTAAAGGTGTCAGAGTGAAGTTCGAGAGTCTGGAG 82
Qy 112 GAGGCTTGTCGAACCTGAGAGTCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 171
Db 83 GAGGCTTGTCGAACCTGAGAGTCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 142
Qy 172 TCAGTGGCTACTGGATCTCTTGGTCCGCCAGTCTCCAGAGAGGGCTTGAGTGGGTG 231
Db 143 TTAGTGATCGCTGGATGGAGTGGGTCGCCAGTCTCCAGAGAGGGCTTGAGTGGGTG 202
Qy 232 CTGAATTAGATTGAATCTGTAATATGCAACACATTATCGGAGTCTGTGAAGGGA 291
Db 203 CTGAATTAGAACAAGCCATATCATGCAACATATATGATGATGCTGTGAAGGGA 262
Qy 292 AGTTACCATCTCAAGAGATGATTCAAAAGTCGCTCTACCTGCAATGAACAGCTTAA 351
Db 263 GGTTCACCATCTCAAGAGATGATTCAAAAGTAGAGTGTACCTGCAATGATTAAGCTTAA 322
Qy 352 GAGCTGAAGACAGTGGAGTTTATTACTGTAC--AGATTTCATAGACTGGGCCCAAGGA 408
Db 323 GAGCTGAAGACAGTGGCCCTTATTACTGTACTGGGAGTTTGTCTAACTGGGCCCAAGGA 382
Qy 409 CACTAGT 415
Db 383 CTCTGGT 389

RESULT 5
US-08-976-288A-12
Sequence 12, Application US/08976288A
Patent No. 6315997
GENERAL INFORMATION:
APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,696
FILING DATE: No. 6315997ember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Anzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6399938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-976-288A-12

Query Match 64.9%; Score 269.4; DB 4; Length 403;
Best Local Similarity 85.3%; Pred. No. 6.2e-72;
Matches 313; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
Qy 52 TTTTATTTATTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGTTCGAGAGTCTGGAG 111
Db 23 TCTCATAGTTTCTTTCTTAAAGGTGTCAGAGTGAAGTTCGAGAGTCTGGAG 82
Qy 112 GAGGCTTGTCGAACCTGAGAGTCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 171
Db 83 GAGGCTTGTCGAACCTGAGAGTCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 142
Qy 172 TCAGTGGCTACTGGATCTCTTGGTCCGCCAGTCTCCAGAGAGGGCTTCAGTGGGTG 231
Db 143 TTAGTGATCGCTGGATGGAGTGGGTCGCCAGTCTCCAGAGAGGGCTTCAGTGGGTG 202
Qy 232 CTGAATTAGATTGAATCTGTAATATGCAACACATTATGCGAGTCTGTGAAGGGA 291
Db 203 CTGAATTAGAACAAGCCATATCATGCAACATATATGATGATGCTGTGAAGGGA 262

```
QY 292 AGTTCCACATCTCAAGAGATGATTCACAAAGTCGTCTCTACCTGCAATGAACAGCTTAA 351
      |||||||
Db 263 GCTTCACCATCTCAAGAGATGATTCACAAAGTAGAGTCTACCTGCAATGAACAGCTTAA 322
      |||||||
QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTAC---AGATTTCATAGACTGGGGCCCAAGGGA 408
      |||||||
Db 323 GAGCTGAAGACACTGGCGCTTTATTACTGTACTGGGAGTTTGCTAACTGGGGCCAGGGA 382
      |||||||
QY 409 CACTAGT 415
      ||||
Db 383 CTCTGGT 389

RESULT 6
US-08-767-128-27
; Sequence 27, Application US/08767128
; Patent No. 611079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USE1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 360 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
```

```
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...360
; OTHER INFORMATION:
; US-08-767-128-27

Query Match 64.5%; Score 267.8; DB 3; Length 360;
Best Local Similarity 92.7%; Pred. No. 1.8e-71;
Matches 281; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGGAGGCTTGGTCCAACTGGAGGATCCATGAACCTC 146
      |||||||
Db 1 GAAGTGAAGACTGAGGAGTCTGGAGGAGGCTTGGTTCACCTGGAGGATCCATGAACCTC 60
      |||||||
QY 147 TCGTGTAGCCTCTGGATTACTTTTCAGTGGCTACTTGGATGCTCTTGGTCCGCCAGTCT 206
      |||||||
Db 61 TCGTGTGTTGCCCTCTGGATTCACTTTTCAGTAACTACTTGGATGAAGTGGTCCGCCAGTCT 120
      |||||||
QY 207 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATAGATTCAAACTCTGATAATTATGCAACA 266
      |||||||
Db 121 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATAGATTGAAATCTAAATAATTATGCAACA 180
      |||||||
QY 267 CATTATGCGGAGTCTGTGAAAGGGAAGTTTCACCATCTCAAGAGATGATTCACAAAAGTCGT 326
      |||||||
Db 181 CATTATGCGGAGTCTGTGAAAGGGAAGTTTCACCATCTCAAGAGATGATTCACAAAAGTAGT 240
      |||||||
QY 327 CTCTACTCCAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
      |||||||
Db 241 GTCTACTCCAAATGAACAACTTAAGAGCTGAAGACAGTGGCAATTTATTACTGTACCGGT 300
      |||||||
QY 387 TTC 389
      ||
Db 301 TAC 303
      ||

RESULT 7
US-08-483-749A-1
; Sequence 1, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
;
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..366
US-08-483-749A-1

Query Match 64.4%; Score 267.2; DB 3; Length 366;
Best Local Similarity 93.9%; Pred. No. 2.7e-71;
Matches 278; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 87 GAAGTGAAGCTTGAGGAGCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAACATC 146
Db 1 GAAGTGAAGCTTGAGGAGCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAACATC 60
QY 147 TCCTGTGTAGCTCTGGATTTACTTTTCAGTGGCTACTGGATGCTTGGTCCGCCAGTCT 206
Db 61 TCCTGTGTAGCTCTGGATTTACTTTTCAGTGGCTACTGGATGCTTGGTCCGCCAGTCT 120
QY 207 CCAGAGAAGGGCTTGAGTGGTTCGCTGAATAGATTGAATGAATATGCAACA 266
Db 121 CCAGAGAAGGGCTTGAGTGGTTCGCTGAATAGATTGAATGAATATGCAACA 180
QY 267 CATTATCGGAGCTCTGTAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCGT 326
Db 181 CATTATCGGAGCTCTGTAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTAGT 240
QY 327 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTAC 382
Db 241 GTCTACCTGCAAACTGAACACTTAAGAGCTGAAGACAGTGGCATTTATTACTGTGC 296

RESULT 8
US-09-318-661-1
; Sequence 1, Application US/09318661
; Patent No. 6268488
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/318,661
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 899
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-318-661-1

Query Match 63.5%; Score 263.6; DB 4; Length 899;
Best Local Similarity 90.6%; Pred. No. 4.5e-70;
Matches 281; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 87 GAAGTGAAGCTTTGAGGAGCTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAACATC 146
Db 434 GAGGTGATGTTGGTGGAGCTCTGGAGGAGGCTTGGTCAACCTGGAGGATCCATGAACATC 375
QY 147 TCCTGTGTAGCTCTGGATTTACTTTTCAGTGGCTACTGGATGCTTGGTCCGCCAGTCT 206
Db 374 TCCTGTGAATTTCTGGATTAATTTTCAGAAATTTATGGATGCTTGGTCCGCCAGTCT 315
QY 207 CCAGAGAAGGGCTTGAGTGGTTCGCTGAATAGATTGAATTCGAATATGCAACA 266
Db 314 CCAGAGAAGGGCTTGAGTGGTTCGCTGAATAGATTGAATTCGAATATGCAACA 255
QY 267 CATTATCGGAGCTCTGTAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCGT 326
Db 254 CATTATCGGAGCTCTGTAAGGGAAGTTCACCATCTCAAGAGATGATTCCAAAGTCGT 195
QY 327 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGAGTGGAGTTTATTACTGTACAT 386
Db 194 CTCTACCTGCAAAATGAACAGCTTAAGAGCTGAAGAGTGGAGTTTATTACTGTACAT 135
QY 387 TTCATAGACT 396
Db 134 TATTTTACT 125

RESULT 10
US-07-977-696C-65
; Sequence 65, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; for Carcinomas and Kit and Diagnostic Vaccination
```

```

; TITLE OF INVENTION: and Therapeutic Methods.
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/977,696C
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66.38227
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6868
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-977-696C-65

```

```

Query Match      63.4%; Score 263; DB 1; Length 403;
Best Local Similarity 84.2%; Pred. No. 5.2e-70;
Matches 309; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

QY 52 TTTTATTTATGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 111
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 23 TCTTCATAGTTTCTCTTAAAGGTGTCAGAGTGAAGTGCAGCTTGTGGAGTCTGGAG 82

QY 112 GAGGCTTGGTCAACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 83 GAGGCTTGGTCAACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 142

QY 172 TCAGTGGCTACTGATGCTTGGGTCCGCGAGTCCAGAGAGGGGCTTGAGTGGGTTG 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 143 TTAGTGATGCTGTGATGAGTGGGTCCGCGAGTCCAGAGAGGGGCTTGAGTGGGTTG 202

QY 232 CTGAATTTAGATTGAATCTGATAATTATGCAACACATTTATGGCGAGTCTGTGAAAGGGA 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 203 CTGAATTTAGAAACAAGCCAATATCATGCAACATATTATGATGAGTCTGTGAAAGGGA 262

QY 292 AGTTCCACATCTCAAGAGATGATTCCAAAAGTGTCTCTACCTGCAAAATGAACAGCTTAA 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 263 GGTTCACCATCTCAAGAGATGATTCCAAAAGTGTCTCTACCTGCAAAATGAACAGCTTAA 322

QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTAC---AGATTTCATAGACTGGGCCCAAGGGA 408
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 323 GAGCTGAAGACACTGCCCTTTATTACTGTACTGGGGAGTTTGTACTGGGCCCAAGGGA 382

QY 409 CACTAGT 415
   ||| |||
DB 383 CTCGTGT 389

```

RESULT 11

```

US-08-129-930B-65
; Sequence 65, Application US/08129930B
; Patent No: 5804187
; GENERAL INFORMATION:

```

```

; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-129-930B-65

```

```

Query Match      63.4%; Score 263; DB 1; Length 403;
Best Local Similarity 84.2%; Pred. No. 5.2e-70;
Matches 309; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

QY 52 TTTTATTTATGTTCTTTTAAAGGGTCCAGAGTGAAGTGAAGCTTGAGGAGTCTGGAG 111
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 23 TCTTCATAGTTTCTCTTAAAGGTGTCAGAGTGAAGTGCAGCTTGTGGAGTCTGGAG 82

QY 112 GAGGCTTGGTCAACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 171
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 83 GAGGCTTGGTCAACCTGGAGGATCCATGAACCTCTCTGTGTAGCTCTGGATTACTT 142

QY 172 TCAGTGGCTACTGATGCTTGGGTCCGCGAGTCCAGAGAGGGGCTTGAGTGGGTTG 231
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 143 TTAGTGATGCTGTGATGAGTGGGTCCGCGAGTCCAGAGAGGGGCTTGAGTGGGTTG 202

QY 232 CTGAATTTAGATTGAATCTGATAATTATGCAACACATTTATGGCGAGTCTGTGAAAGGGA 291
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 203 CTGAATTTAGAAACAAGCCAATATCATGCAACATATTATGATGAGTCTGTGAAAGGGA 262

QY 292 AGTTCCACATCTCAAGAGATGATTCCAAAAGTGTCTCTACCTGCAAAATGAACAGCTTAA 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 263 GGTTCACCATCTCAAGAGATGATTCCAAAAGTGTCTCTACCTGCAAAATGAACAGCTTAA 322

QY 352 GAGCTGAAGACAGTGGAGTTTATTACTGTAC---AGATTTCATAGACTGGGCCCAAGGGA 408
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 323 GAGCTGAAGACACTGCCCTTTATTACTGTACTGGGGAGTTTGTACTGGGCCCAAGGGA 382

QY 409 CACTAGT 415
   ||| |||
DB 383 CTCGTGT 389

```

RESULT 12
US-08-976-288A-65
; Sequence 65, Application US/08976288A
; Patent No. 6315997
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976.288A
; FILING DATE: No. 6315997/ember 21, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/129,930
; FILING DATE: September 30, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,696
; FILING DATE: No. 6315997/ember 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel Ph.D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P6639938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 403 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-976-288A-65

Query Match 63.4%; Score 263; DB 4; Length 403;
Best Local Similarity 84.2%; Pred. No. 5.2e-70;
Matches 309; Conservative 0; Mismatches 55; Indels 3; Gaps 1;
QY 52 TTTTCTTTTATCTCTTTTAAAGGGTCCAGAGTGAAGTCAAGCTTGAGGAGTCTGGAG 111
Db 23 TCTTCATAGTTTCTCTTAAAGGTGTCAGAGTGAAGTCAAGCTTGAGGAGTCTGGAG 82
QY 112 GAGGCTTGGTGCACCTCGAGGATCCATGAACCTCTCCTGTGTAGCCTCTCGATTACTT 171
Db 83 GAGGCTTGGTGCACCTCGAGGATCCATGAGACTCTCTGTGTCTCTCGATTACTT 142
QY 172 TCAGTGGCTACGAGATGCTTGGGTCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTG 231
Db 143 TTAGTGATGCCTGGATGACTGGGTCCGCCAGTCTCCAGGAAGGGGCTTGAGTGGGTG 202
QY 232 CTGAATTTAGATTGAATCTGATTAATATGCAACATTATTCGGAGTCTGTGAAGGGA 291
|||||

Db 203 CTGAAATTAGAAACAAAGCCAAATAATCATGCAACATATTATGATGAGTCTGTGAAAGGA 262
QY 292 AGTTCACCATCTCAAGAGATGATTCCAAAGTCGTCTCTACCTGCAAAATGAACAGCTTAA 351
Db 263 GGTTCACCATCTCAAGAGATGATTCCAAAGTACTGTGTACCTGCAAAATGAATAGCTTAA 322
QY 352 GAGCTGAAGACAGCTGGAGTTTATTACTGTAC---AGATTTTCATAGACTGGGCCAAGGA 408
Db 323 GAGCTGAAGACACTGCCCTTTATTACTGTACTGTGAGGAGTTTGTCTACTGGGCCAGGGA 382
QY 409 CACTAGT 415
Db 383 CTCTGGT 389
RESULT 13
US-08-483-749A-9
; Sequence 9, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..342
US-08-483-749A-9
Query Match 62.4%; Score 259; DB 3; Length 342;
Best Local Similarity 87.6%; Pred. No. 7.8e-69;
Matches 283; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 87 GAAGTGAAGCTTGAGGAGTCTGGAGAGGCTTGGTCAACCTGGAGATCCATGAACATC 146
Db 1 GAGGTGAACCTTGAGGAGTCTGGAGAGGCTTGGTCAACCTGGAGATCTATGAACATC 60
QY 147 TCCTGTGTACCTCTGGATTACTTTCAGTGGCTACTGGATGCTTGGGTCCGCCAGTCT 206
Db 61 TCCTGTGTTCCTCTGGATTCACTTTCAGTGAATTTGGATGAATTTGGGTCCGCCAGTCT 120
QY 207 CCAGAGAAGGGCTTGAGTGGTGGTGAATTTAGATTTGAATTTGAATTTGAATTTGAATTT 266
Db 121 CCAGAGAAGGGCTTGAGTGGTGGTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTT 180

```
;
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...357
; OTHER INFORMATION:
; US-08-767-128-25

Query Match      61.8%; Score 256.6; DB 3; Length 357;
Best Local Similarity 92.7%; Pred. No. 4.2e-68;
Matches 281; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 267 CATTATGGGAGTCTGTGAAGGAGGAGTTCACCATCTCAAGAGATGATTCACAAAGTCGT 326
Db 181 CATTATGGGAGTCTGTGAAGGAGGAGTTCACCCCTCAAGAGATGATTCACAAAGTAGT 240
QY 327 CTCCTACCTGCAATGACACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
Db 241 ATCTACCTGCAATGAATACTTAAGAACTGAAGACACTGGCATTATTCTCTGACGTTTC 300
QY 387 TTCATAGACTGGGCCCAAGGCAC 409
Db 301 TGGGACTATTGGGCCCGAGGCAC 323

RESULT 14
US-08-767-128-25
; Sequence 25, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 357 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
```

```
;
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...357
; OTHER INFORMATION:
; US-08-767-128-25

Query Match      61.8%; Score 256.6; DB 3; Length 357;
Best Local Similarity 92.7%; Pred. No. 4.2e-68;
Matches 281; Conservative 0; Mismatches 19; Indels 3; Gaps 1;

QY 87 GAAGTGAAGCTTGAAGAGTCTGGAGGAGGCTTGGTGCACACCTGGAGGATCCATGAACTC 146
Db 1 GAAGTTAAGCTTGAAGAGTCTGGAGGAGGCTTGGTGCACACCTGGAGGATCCATGAACTC 60
QY 147 TCCTGTGTAGCCTCTGGATTACTTTTTCAGTGGCTACTGGATGCTCTTGGGTCGCCAGTCT 206
Db 61 TCCTGTGTGGCCTCTGGATTACTTTTTCAGTAACTACTGGATGAACCTGGGTCGCCAGTCT 120
QY 207 CCAGAGAAGGGGCTTGAAGTGGGTTGCTGAAATTAAGATTGAATCTGATAATTATGCAACA 266
Db 121 CCAGAGAAGGGGCTTGAAGTGGGTTGCTGAAATTAAGATTGAATCTGATAATTATGCAACA 177
QY 267 CATTATGGGAGTCTGTGAAGGAGGAGTTCACCATCTCAAGAGATGATTCACAAAGTCGT 326
Db 178 CATTATGGGAGTCTGTGAAGGAGGAGTTCACCATCTCAAGAGATGATTCACAAAGTAGT 237
QY 327 CTCCTACCTGCAATGAACAGCTTAAGAGCTGAAGACAGTGGAGTTTATTACTGTACAGAT 386
Db 238 GTCCTACCTGCAATGAACAACTTAAGAGCTGAAGACACTGGAATTTATTACTGTACCGGT 297
QY 387 TTC 389
Db 298 TAC 300

RESULT 15
US-08-192-102-4
; Sequence 4, Application US/08192102
; Patent No. 5656272
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter E.
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott A.
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND ASSAYS EMPLOYING
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/192,102
; FILING DATE: 04-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/192,093
; FILING DATE: 04-FEB-1994
; APPLICATION NUMBER: US 08/013,413
; FILING DATE: 02-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010,406
```

	Query Match	61.78;	Score 256;	DB 1;	Length 357;
	Best Local Similarity	91.66;	Pred. No. 6.3e-68;		
	Matches 271;	Conservative	0;	Mismatches 25;	Indels 0;
				Gaps	0;
QY	87	GAAGTGAAGCTTGAAGAGCTCGGAGGAGGCTTGTCACACTGGAGGATCCATGAACATC	146		
Db	1	GAAGTGAAGCTTGAAGAGCTCGGAGGAGGCTTGTCACACTGGAGGATCCATGAACATC	60		
QY	147	TCCTGTGTAGCCCTCGGATTTACATTCAGTGGCTACTGGATGCTTTGGGTCCGCCAGTCT	206		
Db	61	TCCTGTGTGTGCTCGGATTCATTTTCAGTACCACCTGGAGTGGGTCCGCCAGTCT	120		
QY	207	CCAGAGAAGGGCTTGTAGTGGTTCGTGAATTAGATTGAATTCGATTAATTATGCAACA	266		
Db	121	CCAGAGAAGGGCTTGTAGTGGTTCGTGAATTAGATCAAAATCTATTATTCTGCAACA	180		
QY	267	CATTATGCGGAGCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCGT	326		
Db	181	CATTATGCGGAGCTGTGAAAGGGAAGTTCACCATCTCAAGAGATGATTCCTCAAAAGTCGT	240		
QY	327	CTCTACTGCAATTGAACAGCTTAAGAGCTCAAGACAGTGGAGTTCCTATTACTGTAC	392		
bb	241	GTCTACTGCAATTGAACAGCTTAAGAGCTCAAGACAGTGGAGTTCCTATTACTGTAC	296		

Search completed: April 26, 2003, 07:28:34
Job time : 20.1893 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: April 26, 2003, 04:53:31 ; Search time 872.104 Seconds
(without alignments)
14583.043 Million cell updates/sec

Title: US-09-674-716B-2
Perfect score: 437
Sequence: 1 aagctttacagttactcagc.....agttggaaataaaacgtacg 437

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues 4109280
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.or.*
- 21: em.ov.*
- 22: em.pat.*
- 23: em.ph.*
- 24: em.pl.*
- 25: em.ro.*
- 26: em.sts.*
- 27: em.un.*
- 28: em.vi.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	437	100.0	437	6	AX010601	AX010601 Sequence
c	437	100.0	437	6	AX010644	AX010644 Sequence
3	373.2	85.4	431	10	MUSIGKONG	M19910 Mouse Ig re
4	371.6	85.0	458	10	MUSIGKCNF	J09509 Mouse Ig re
5	333.4	76.3	1400	10	MUSIGRAH	J09553 Mouse Ig ka
6	326.8	74.8	339	10	MMU29425	U29425 Mus musculus
7	317.2	72.6	339	6	AR072863	AR072863 Sequence
8	317.2	72.6	339	6	AR166313	AR166313 Sequence
9	317.2	72.6	368	6	AR072861	AR072861 Sequence
10	317.2	72.6	368	6	AR166317	AR166317 Sequence
11	316	72.3	420	6	AR166319	AR166319 Sequence
12	309.2	70.8	368	6	AR072865	AR072865 Sequence
13	309.2	70.8	368	6	AR166315	AR166315 Sequence
14	308	70.5	825	10	MMIG28	V00779 Mouse immun
15	308	70.5	899	10	MMU231264	AJ231264 Mus muscu
16	308	70.5	1047	10	MUSIGKVH2	J00562 Mouse Ig ka
17	308	70.5	1060	10	MUSIGKVT1	K02415 Mouse Ig ge
c	308	70.5	63428	2	AC101099	AC101099 Mus muscu
c	308	70.5	208895	2	AC122322	AC122322 Mus muscu
18	296.8	67.9	1149	10	MUSIGKVAA	M80407 Mouse Ig ge
20	293.6	67.2	396	10	MMU277812	AJ277812 Mus muscu
21	293.2	67.1	464	6	A29573	A29573 M.musculus
22	293.2	67.1	464	6	I25724	I25724 Sequence 15
23	293.2	67.0	451	10	MMSV5PKL	Z49934 M.musculus
24	292.6	67.0	451	10	AF045509	AF045509 Mus muscu
25	288.8	66.1	396	10	AF045509	E08433 cDNA encodi
26	286.8	65.6	961	6	E08433	E08433 Mouse germl
27	286.4	65.5	978	10	MUSIGKVN	M15553 Mouse germl
28	284.4	65.1	399	10	MMU202070	U202070 Mus muscu
29	284	65.1	982	10	MUSIGKVNA	M15552 Mouse germl
30	284	65.0	396	10	AF045515	AF045515 Mus muscu
31	280	64.1	593	10	MMIGM65A	X57856 M.musculus
32	276.4	63.2	399	6	A23299	A23299 M.musculus
33	276.4	63.2	399	6	AR013733	AR013733 Sequence
34	275.2	63.0	993	10	AF466768	AF466768 Mus muscu
35	262.2	60.0	339	10	AF087033	AF087033 Mus muscu
36	257.2	58.9	348	6	AX010614	AX010614 Sequence
c	257.2	58.9	348	6	AX010645	AX010645 Sequence
37	256.2	58.6	163929	2	AC118484	AC118484 Rattus no
38	255.6	58.5	720	6	E35205	E35205 Human monoc
39	255.6	58.5	720	6	E35208	E35208 Human monoc
40	254.6	58.3	720	6	E35207	BC030814 Homo sapi
41	253.4	58.0	972	9	BC030814	E35207 Human monoc
42	253	57.9	720	6	E35207	E35207 Human monoc
c	253	57.9	5541	2	AC098332	AC098332 Rattus no
43	252.6	57.8	405	9	HSKPOLC01	Z68925 H.sapiens m
44	252.6	57.8	405	9	HSKPOLC01	Z68925 H.sapiens m
45	252.2	57.7	410	9	HSIGKLV46	X72467 H.sapiens m

ALIGNMENTS

RESULT 1	AX010601	AX010601	Sequence 2 from Patent WO9958679.	437 bp	DNA	linear	PAT 06-SEP-2000
LOCUS	AX010601	AX010601	Sequence 2 from Patent WO9958679.	437 bp	DNA	linear	PAT 06-SEP-2000
DEFINITION	AX010601	AX010601	Sequence 2 from Patent WO9958679.	437 bp	DNA	linear	PAT 06-SEP-2000
ACCESSION	AX010601	AX010601	Sequence 2 from Patent WO9958679.	437 bp	DNA	linear	PAT 06-SEP-2000
VERSION	AX010601.1	AX010601.1	GI:9997413	437 bp	DNA	linear	PAT 06-SEP-2000
KEYWORDS	house mouse.	house mouse.	house mouse.	437 bp	DNA	linear	PAT 06-SEP-2000
SOURCE	house mouse.	house mouse.	house mouse.	437 bp	DNA	linear	PAT 06-SEP-2000
ORGANISM	Mus musculus	Mus musculus	Mus musculus	437 bp	DNA	linear	PAT 06-SEP-2000
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	437 bp	DNA	linear	PAT 06-SEP-2000
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	437 bp	DNA	linear	PAT 06-SEP-2000
TITLE	1 (bases 1 to 437)	1 (bases 1 to 437)	1 (bases 1 to 437)	437 bp	DNA	linear	PAT 06-SEP-2000
JOURNAL	Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.	Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.	Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.	437 bp	DNA	linear	PAT 06-SEP-2000
	Antibodies to cd23, derivatives thereof, and their therapeutic uses	Antibodies to cd23, derivatives thereof, and their therapeutic uses	Antibodies to cd23, derivatives thereof, and their therapeutic uses	437 bp	DNA	linear	PAT 06-SEP-2000
	Patent: WO 9958679-A 2 18-NOV-1999;	Patent: WO 9958679-A 2 18-NOV-1999;	Patent: WO 9958679-A 2 18-NOV-1999;	437 bp	DNA	linear	PAT 06-SEP-2000

BONNEFOY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY (GB); SHEARIN JEAN (US)

Location/Qualifiers
1. 437
/organism="Mus musculus"
/db_xref="taxon:10090"

BASE COUNT 108 a 93 c 114 g 122 t

ORIGIN

Query Match 100.0%; Score 437; DB 6; Length 437;
Best Local Similarity 100.0%; Pred. No. 9.4e-133;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTCAGTTTCTGG 60
DB 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTCAGTTTCTGG 60
QY 61 GGGTGGTTATGTTCTGGATCTCTGGAGTCAGTGGGATATTGTGATAACCCAGGATGAAC 120
DB 61 GGGTGGTTATGTTCTGGATCTCTGGAGTCAGTGGGATATTGTGATAACCCAGGATGAAC 120
QY 121 TCTCCAATCCTCTGATCTCTGGAGTCACTGAGTGGGATATTGTGATAACCCAGGATGAAC 180
DB 121 TCTCCAATCCTCTGATCTCTGGAGTCACTGAGTGGGATATTGTGATAACCCAGGATGAAC 180
QY 181 TCTGTTAAGGATGGGAGACATCTTGAATTTGTTCTGCAGAGACAGGACATCTC 240
DB 181 TCTGTTAAGGATGGGAGACATCTTGAATTTGTTCTGCAGAGACAGGACATCTC 240
QY 241 CTCAGTCTCTGATGTTATGTTGATGTTCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTG 300
DB 241 CTCAGTCTCTGATGTTATGTTGATGTTCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTG 300
QY 301 GCAGTGGGTGAGGACAGATTTCACCCCTGGAAATCAGTAGAGTGAAGCTGAGGATGTGG 360
DB 301 GCAGTGGGTGAGGACAGATTTCACCCCTGGAAATCAGTAGAGTGAAGCTGAGGATGTGG 360
QY 361 GTGTGTTATTTGTTCAACAACCTTTGAGAGTATCCATTCCAGTTCCGGCTCGGGGACAAAGT 420
DB 361 GTGTGTTATTTGTTCAACAACCTTTGAGAGTATCCATTCCAGTTCCGGCTCGGGGACAAAGT 420
QY 421 TGGAAATAAACGCTAGC 437
DB 421 TGGAAATAAACGCTAGC 437

RESULT 2
AX010644/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
MEDLINE
PUBMED
COMMENT
FEATURES
source

AX010644
Sequence 47 from Patent WO9958679.
AX010644
AX010644.1 GI:9997453
house mouse.
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 437)
Bonney, J.Y., Crowe, S.J., Rapson, N.T., Ellis, J.H. and Shearin, J.
Antibodies to cd23, derivatives thereof, and their therapeutic uses
Patent: WO 9958679-A 47 18-NOV-1999;
BONNEFOY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY (GB); SHEARIN JEAN (US)

Location/Qualifiers
1. 437
/organism="Mus musculus"
/db_xref="taxon:10090"

BASE COUNT 122 a 114 c 93 g 108 t

ORIGIN

Query Match 100.0%; Score 437; DB 6; Length 437;
Best Local Similarity 100.0%; Pred. No. 9.4e-133;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTCAGTTTCTGG 60
DB 437 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGGTTCTCTGTTCAGTTTCTGG 378
QY 61 GGGTGGTTATGTTCTGGATCTCTGGAGTCAGTGGGATATTGTGATAACCCAGGATGAAC 120
DB 377 GGGTGGTTATGTTCTGGATCTCTGGAGTCAGTGGGATATTGTGATAACCCAGGATGAAC 318
QY 121 TCTCCAATCCTCTGATCTCTGGAGTCACTGAGTGGGATATTGTGATAACCCAGGATGAAC 180
DB 317 TCTCCAATCCTCTGATCTCTGGAGTCACTGAGTGGGATATTGTGATAACCCAGGATGAAC 258
QY 181 TCTGTTAAGGATGGGAGACATCTTGAATTTGTTCTGCAGAGACAGGACATCTC 240
DB 257 TCTGTTAAGGATGGGAGACATCTTGAATTTGTTCTGCAGAGACAGGACATCTC 198
QY 241 CTCAGTCTCTGATGTTATGTTGATGTTCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTG 300
DB 197 CTCAGTCTCTGATGTTATGTTGATGTTCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTG 138
QY 301 GCAGTGGGTGAGGACAGATTTCACCCCTGGAAATCAGTAGAGTGAAGCTGAGGATGTGG 360
DB 137 GCAGTGGGTGAGGACAGATTTCACCCCTGGAAATCAGTAGAGTGAAGCTGAGGATGTGG 78
QY 361 GTGTGTTATTTGTTCAACAACCTTTGAGAGTATCCATTCCAGTTCCGGCTCGGGGACAAAGT 420
DB 77 GTGTGTTATTTGTTCAACAACCTTTGAGAGTATCCATTCCAGTTCCGGCTCGGGGACAAAGT 18
QY 421 TGGAAATAAACGCTAGC 437
DB 17 TGGAAATAAACGCTAGC 1

RESULT 3
MUSIGKNG
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
MEDLINE
PUBMED
COMMENT
FEATURES
source

MUSIGKNG
Mouse Ig rearranged kappa-chain mRNA, clone AN06K.
M19910.1 J03832
M19910.1 GI:197027
C-region: immunoglobulin light chain; immunoglobulin-kappa;
processed gene.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 56)
Rule, G.S.
Unpublished (1988)
2 (bases 1 to 431)
Leahy, D.J., Rule, G.S., Whittaker, M.M. and McConnell, H.M.
Sequences of 12 monoclonal anti-dinitrophenyl spin-label antibodies
for NMR studies
Proc. Natl. Acad. Sci. U.S.A. 85 (11), 3661-3665 (1988)
3375235
Draft entry and computer-readable sequence [2] kindly submitted by
G. Rule, 20-JUL-1988.
Location/Qualifiers
1. 431
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"

```
/db_xref="taxon:10090"
/cell_type="mature B cell"
32..>431
/feature="precursor"
/codon_start=1
/product="immunoglobulin kappa-chain"
/protein_id="AAA38885.1"
/db_xref="GI:554111"
/translaton="MRC5LOFLGVLMEFISGSDIVITODELSNPVTSGESVSISCR
STKSLLYKDKTYLWFLORPGQSPOLLYLMSTRASGVSDRSGSGSGTDFLEISR
VKAEDEVVYVYCOQLVEFLPFGAGTKLELR"
32..91
sig_peptide
mat_peptide
92..>431
/product="immunoglobulin kappa-chain"
BASE COUNT 103 a 96 c 113 g 119 t
ORIGIN
Query Match 85.4%; Score 373.2; DB 10; Length 431;
Best Local Similarity 94.4%; Pred. No. 1.1e-111;
Matches 387; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 24 CAGGACCTCACCAGTCTCTGTTTCAGTTTCTGGGGTGCCTATGTTCTGATCTCT 83
II I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 20 CAAGTTCTCAGATGAGTCTCTCTTCAGTTCTGGGGTGCCTATGTTCTGATCTCT 79
QY 84 GAGTCACTGGGATATTGTGATACCCAGGATGAATCTCCAATCCTGCTCTCTGGA 143
II I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 80 GAGTCACTGGGATATTGTGATACCCAGGATGAATCTCCAATCCTGCTCTCTGGA 139
QY 144 GAATCAGTTTCCATCTCTCGAGTCTAGTAAAGTCTCTCTGATAGGATGGGAAGACA 203
II I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 140 GAATCAGTTTCCATCTCTCGAGTCTAGTAAAGTCTCTCTGATAGGATGGGAAGACA 199
QY 204 TACTTGAATGGTTTCTCAGAGACCCAGGACAACTCTCTCAGCTCTGATATTGATG 263
II I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 200 TACTTGAATGGTTTCTCAGAGACCCAGGACAACTCTCTCAGCTCTGATATTGATG 259
QY 264 TCCACCCGTGATCAGGAGTCTCAGACCGTTTGTAGTGGCAGTGGGTGAGGACAGATTC 323
II I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 260 TCCACCCGTGATCAGGAGTCTCAGACCGTTTGTAGTGGCAGTGGGTGAGGACAGATTC 319
QY 324 ACCCTGGAATCAGTAGAGTGAAGCTGAGGATGGGTGTGTTATTCTGTCACAACTT 383
II I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 320 ACCCTGGAATCAGTAGAGTGAAGCTGAGGATGGGTGTGTTATTCTGTCACAACTT 379
QY 384 GTAGAGTATCCATTACCTTCGCTCGGGGACAAAGTTGGAATAAAGC 433
II I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 380 GTAGAGTTCGGCTCACGTTCCGTTCTGGGACCAAGCTGGAGCTGAAAGC 429
RESULT 4
MUSIGKCNF 458 bp mRNA linear ROD 26-MAR-1994
LOCUS Mouse Ig rearranged kappa-chain mRNA, clone AN05K.
DEFINITION M19909 J03832
ACCESSION M19909.1
VERSION GI:197025
KEYWORDS C-region; immunoglobulin light chain; immunoglobulin-kappa; processed gene.
SOURCE Mus musculus
ORGANISM Mus musculus (strain BALB/c, sub_species domesticus) cDNA to mRNA.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 56)
REFERENCE Rule, G.S.
AUTHORS Unpublished (1988)
REFERENCE 2 (bases 1 to 458)
AUTHORS Leahy, D.J., Rule, G.S., Whittaker, M.M. and McConnell, H.M.
TITLE Sequences of 12 monoclonal anti-dinitrophenyl spin-label antibodies for NMR studies
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (11), 3661-3665 (1988)
MEDLINE 88234486
PUBMED 3375235
COMMENT Draft entry and computer-readable sequence [2] kindly submitted by
```

```
G.Rule, 20-JUL-1988.
Location/Qualifiers
source 1..458
/organism="Mus musculus"
/strain="BALB/c"
/sub_species="domesticus"
/db_xref="taxon:10090"
/cell_type="mature B cell"
44..>458
CDS
/feature="precursor"
/codon_start=1
/product="immunoglobulin kappa-chain"
/protein_id="AAA38884.1"
/db_xref="GI:554110"
/translaton="MRC5LOFLGVLMEFISGSDIVITODELSNPVTSGESVSISCR
STKSLLYKDKTYLWFLORPGQSPOLLYLMSTRASGVSDRSGSGSGTDFLEISR
VKAEDEVVYVYCOQLVEFLPFGAGTKLELR"
44..103
sig_peptide
mat_peptide
104..>458
/product="immunoglobulin kappa-chain"
BASE COUNT 108 a 105 c 119 g 126 t
ORIGIN
Query Match 85.0%; Score 371.6; DB 10; Length 458;
Best Local Similarity 94.1%; Pred. No. 3.6e-111;
Matches 386; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 24 CAGGACCTCACCAGTCTCTGTTTCAGTTTCTGGGGTGCCTATGTTCTGATCTCT 83
II I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 32 CAAGTTCTCAGATGAGTCTCTCTTCAGTTCTGGGGTGCCTATGTTCTGATCTCT 91
QY 84 GAGTCACTGGGATATTGTGATACCCAGGATGAATCTCCAATCCTGCTCTCTGGA 143
II I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 92 GAGTCACTGGGATATTGTGATACCCAGGATGAATCTCCAATCCTGCTCTCTGGA 151
QY 144 GAATCAGTTTCCATCTCTCGAGTCTAGTAAAGTCTCTCTGATAGGATGGGAAGACA 203
II I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 152 GAATCAGTTTCCATCTCTCGAGTCTAGTAAAGTCTCTCTGATAGGATGGGAAGACA 211
QY 204 TACTTGAATGGTTTCTCAGAGACCCAGGACAACTCTCTCAGCTCTGATATTGATG 263
II I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 212 TACTTGAATGGTTTCTCAGAGACCCAGGACAACTCTCTCAGCTCTGATATTGATG 271
QY 264 TCCACCCGTGATCAGGAGTCTCAGACCGTTTGTAGTGGCAGTGGGTGAGGACAGATTC 323
II I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 272 TCCACCCGTGATCAGGAGTCTCAGACCGTTTGTAGTGGCAGTGGGTGAGGACAGATTC 331
QY 324 ACCCTGGAATCAGTAGAGTGAAGCTGAGGATGGGTGTGTTATTCTGTCACAACTT 383
II I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 332 ACCCTGGAATCAGTAGAGTGAAGCTGAGGATGGGTGTGTTATTCTGTCACAACTT 391
QY 384 GTAGAGTATCCATTACCTTCGCTCGGGGACAAAGTTGGAATAAAGC 433
II I IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII IIII
Db 392 GTAGAGTTCGGCTCACGTTCCGTTCTGGGACCAAGCTGGAGCTGAACG 441
RESULT 5
MUSIGKAH 1400 bp DNA linear ROD 18-APR-1994
LOCUS Mouse Ig kappa active gene: v-kappa-167 v-j region.
DEFINITION J00553 J00563
ACCESSION J00553.1
VERSION GI:196735
KEYWORDS C-region; J-region; V-region; complementarity determining region; framework region; hypervariable region; immunoglobulin light chain; immunoglobulin-kappa; immunoglobulin-kappa subgroup vk-24; processed gene.
SOURCE mouse cDNA to myeloma m167 mrna; hybridomas hpcg9, hpcg10, hpcg13, hpcg22 & myelomas m511, m167 dna (see comment).
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 158 to 170; 537 to 617)
REFERENCE Joho, R., Weissman, I.L., Early, P., Cole, J. and Hood, L.
AUTHORS
```

TITLE Organization of kappa light chain genes in germ-line and somatic tissue

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 77 (2), 1106-1110 (1980)

MEDLINE 80145717

PUBMED 6244580

REFERENCE 2 (bases 159 to 170; 537 to 847)

AUTHORS Gershenfeld,H.K., Tsukamoto,A., Weissman,I.L. and Joho,R.

TITLE Somatic diversification is required to generate the V kappa genes of MOPC 511 and MOPC 167 myeloma proteins

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 78 (12), 7674-7678 (1981)

MEDLINE 82150933

PUBMED 6801657

REFERENCE 3 (bases 1 to 1400)

AUTHORS Gearhart,P.J. and Bogenhagen,D.F.

TITLE Clusters of point mutations are found exclusively around rearranged antibody variable genes

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 80 (11), 3439-3443 (1983)

MEDLINE 83221610

PUBMED 6222379

COMMENT the v-k167 gene codes for a v region which binds phosphocholine. all rearrangements of the v-k167 gene reported here are productive, and in all cases except hybridoma hpcg13 the codon at the site of recombination is ccg. in hpcg13 the codon is cct. the difference could be due to the variability of the v-j recombination site, or it could be an additional somatic mutation. [3] sequenced portions of the j-c intron and the c-kappa gene for all of its hybridomas and myelomas, and found no somatic mutation in these regions. [3] proposes a mechanism for the generation of clustered somatic mutation in the v-j region.

for the germline sequences of the v-k167 v and j regions see <musigkh2> <musigkj2>. see loci beginning <musigka> for other rearranged kappa genes; see loci beginning <musigkv> for germline kappa v regions and see loci beginning <musigkj> for the germline kappa j and c regions. in the sites table cdr-complementarity determining region and fr-framework region.

Complete source information:

mouse cdna to myeloma m167 mrna [1],[2]; hybridomas hpcg9, hpcg10, hpcg13, hpcg22 & myeloma m511, m167 dna [3].

FEATURES

source 1..1400

Location/Qualifiers

1..1400

/organism="Mus musculus"

/db_xref="taxon:10090"

join(123..171,537..884)

/partial

/notes="Ig V-K167 precursor"

/codon_start=1

/protein_id="AAA38770.1"

/db_xref="GI:554091"

/translation="MRCSLQFLGLVLMFWISGVSDIVITQDELSNPVTSGESVSISCR SSKSLYKDGKTYLWNFLORPGSQPOLLIYLMSTRASGVSDRFSGSGCTDFTLEISR VKAEDGVVYCQQLVEYPLTFGAGTKLEUK"

sig_peptide join(123..171,537..847)

mat_peptide /notes="Ig V-K167 signal pept"

548..>883

exon /product="Ig V-K167 mature v-j region"

<123..171

/note="Ig V-K167 precursor"

/number=1

Intron 172..536

/note="-k167 intron a"

283

variation /notes="t in germline; g in hybridoma hpcg13"

320

variation /note="c in germline; g in hybridoma hpcg10"

376

variation /note="a in germline; t in hybridoma hpcg13"

391

variation /note="t in germline; c in hybridoma hpcg13"

409

variation /note="t in germline; c in myeloma m511"

417

variation /note="a in germline; g in myeloma m167"

420

variation

variation /note="a in germline; g in myeloma m167"

440

variation /note="a in germline; g in myeloma m167"

467

variation /note="a in germline; g in hybridoma hpcg13"

515

variation /note="c in germline; a in hybridoma hpcg13"

522

variation /note="t in germline; a in myeloma m511"

525

variation /note="c in germline; t in myeloma m511"

537..>884

/note="Ig V-K167 precursor"

/number=2

550

variation /note="t in germline; c in hybridoma hpcg13"

566

variation /note="g in germline; a in hybridoma hpcg13"

580

variation /note="t in germline; g in myeloma m511"

708

variation /note="a in germline; c in myeloma m167"

727

variation /note="a in germline; c in myeloma m167"

764

variation /note="g in germline; a in myeloma m167"

791

variation /note="a in germline; c in myeloma m167"

846..847

misc_recomb

847

variation /organism="Mus musculus"

895

variation /note="g in hybridomas hpcg9, hpcg10, hpcg22 & comment)

511, m167; t in hybridoma hpcg13(see

859

variation /note="t in germline; c in hybridoma hpcg10"

885..>1400

intron

/note="v-k167 intron j-c"

895

variation /note="t in germline; c in hybridoma hpcg10"

1082

variation /note="a in germline; t in hybridoma hpcg13"

1085

variation /note="c in germline; t in myeloma m167"

1086

variation /note="t in germline; a in hybridoma hpcg10"

1096

variation /note="a in germline; c in hybridoma hpcg13"

1159

variation /note="t in germline; g in hybridoma hpcg10"

1229

variation /note="a in germline; g in hybridoma hpcg13"

1251

variation /note="c in germline; t in myeloma m167"

1260

variation /note="t in germline; g in myeloma m167"

1272

variation /note="c in germline; t in myeloma m167"

1279..1283

variation /note="tgaag in germline; tg in myeloma m511"

1289

variation /note="c in germline; t in hybridoma hpcg10"

BASE COUNT 399 a 250 c 350 g 401 t

ORIGIN unreported, chromosome 6.

Query Match 76.3%; Score 333.4; DB 10; Length 1400;

Best Local Similarity 95.5%; Pred. No. 1.5e-98;

Matches 343; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 79 TCCTGGAGTCAGTGGGATATTGTGATAACCCAGAGTCACTCTCCAACTCTGTCACCTT 138

Db 531 TTTCAGAGTCAGTGGGATATTGTGATAACCCAGAGTCACTCTCCAACTCTGTCACCTT 590

Qy 139 CTGGAGATCAGTTCCATCTCTCGAGGCTGTAGTAAGAGTCTCTGTATAGGATGGGA 198

```

|||||
Db 591 CTGGAGAAATCAGTTTCCATCTCTGCAGGTCTAGTAAGAGTCTCCTATATAAGGATGGGA 650
QY 199 AGACATACCTTGAATTTGTTTCTCAGAGACCAGGACAATCTCCTCAGCTCCTGATCTATT 258
Db 651 AGACATACCTTGAATTTGTTTCTCAGAGACCAGGACAATCTCCTCAGCTCCTGATCTATT 710
QY 259 TGATGTCCACCGGTGCATCAGGAGTCTCAGACCGGTTTGTAGTGCAGTGGTTCAGGACACAG 318
Db 711 TGATGTCCACCGGTGCATCAGGAGTCTCAGACCGGTTTGTAGTGCAGTGGTTCAGGACACAG 770
QY 319 ATTTCACCTTGGAAATCAGTAGAGTGAAGCTCAGGATGGGTGTATTACTGTCAAC 378
Db 771 ATTTCACCTTGGAAATCAGTAGAGTGAAGCTCAGGATGGGTGTATTACTGTCAAC 830
QY 379 AACTTGTAGAGTATCCATTCACGTTCCGGCTCGGGGCAAAAGTTGGAATAAAACGTACG 437
Db 831 AACTTGTAGAGTATCCCTCAGTTCGGTCTGGGACCAAGCTGGAGCTGAACAGTAAG 889

RESULT 6
MMU29425 339 bp mRNA linear ROD 03-FEB-1998
LOCUS Mus musculus anti-PC rearranged Ig kappa chain V-J region mRNA,
DEFINITION hybridoma 31-34-2, partial cds.
ACCESSION U29425
VERSION U29425.1 GI:2745913
KEYWORDS Mus musculus.
SOURCE Mus musculus.
ORGANISM Mus musculus.

REFERENCE
AUTHORS Guo,W.X., Burger,A., Fischer,R.T., Sieckman,D.G., Longo,D.L. and
Kenn,J.J.
TITLE Sequence changes at the V-D junction of the VHL heavy chain of
anti-phosphocholine antibodies alter binding to and protection
against Streptococcus pneumoniae
JOURNAL Int. Immunol. 9 (5), 665-677 (1997)
MEDLINE 97328374
PUBMED 9184912
REFERENCE 2 (bases 1 to 339)
AUTHORS Guo,W.X., Burger,A., Fischer,R.T., Sieckman,D.G., Longo,D.L. and
Kenn,J.J.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-1998) FCRDC, NCI, P.O. Box B, Frederick, MD
21702-1201, USA
REFERENCE 3 (bases 1 to 339)
AUTHORS Guo,W.X., Burger,A., Fischer,R.T., Sieckman,D.G., Longo,D.L. and
Kenn,J.J.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-1998) FCRDC, NCI, P.O. Box B, Frederick, MD
21702-1201, USA
REMARK Nucleotide and protein sequence update by submitter
COMMENT On Jan 5, 1998 this sequence version replaced gi:903959.
FEATURES
source
1..339
/organism="Mus musculus"
/strain="C.CBA/N"
/db_xref="taxon:10090"
/cell_line="hybridoma 31-34-2"
/notes="hybridoma from spleen fused with SP2/0 myeloma"
<1..>339
/notes="vk24/Jk4"
/codon_start=1
/product="anti-PC Ig kappa chain"
/protein_id="AAC00035.1"
/db_xref="GI:2745914"
/translation="DIVITQDELSPVTSGDSVTSISRSKSLLYKDGKTVLNVFLQR
PGSPOLLIVLMSTRASGVSDRFSGSGSDTFLFISRVKPDVGVIYVYCCQLVPEPT
FGSGNKLKLR"
BASE COUNT 90 a 73 c 85 g 91 t
ORIGIN

```

```

Query Match 74.8%; Score 326.8; DB 10; Length 339;
Best Local Similarity 97.9%; Pred. No. 2.1e-96;
Matches 331; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 96 GATATTGTGATAAACCAGGATGAACCTCTCCAATCTGTCACTTCTGGAGAAATCAGTTTCC 155
Db 1 GATATTGTGATAAACCAGGATGAACCTCTCCAATCTGTCACTTCTGGAGAAATCAGTTTCC 60
QY 156 ATCTCCTCAGGTCTAGTAAGAGTCTCCTGTATAGGATGGGAACACATCTTGAATTGG 215
Db 61 ATCTCCTCAGGTCTAGTAAGAGTCTCCTGTATAGGATGGGAACACATCTTGAATTGG 120
QY 216 TTCTTCGAGAGACCAGGACAATCTCCTCAGCTCCTGTATTTGATGTCACCGGTGCA 275
Db 121 TTCTTCGAGAGACCAGGACAATCTCCTCAGCTCCTGTATTTGATGTCACCGGTGCA 180
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGCACAGATTTCCACCTGGAATC 335
Db 181 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGCACAGATTTCCACCTGGAATC 240
QY 336 AGTAGAGTCAAGGCTCAGGATGTTGGTGTATTACTGTCAACAATTTGTAGATATCCA 395
Db 241 AGTAGAGTCAAGGCTCAGGATGTTGGTGTATTACTGTCAACAATTTGTAGATATCCA 300
QY 396 TTCACGTTTCGGCTCGGGGACAAAAGTTGGAATAAAACG 433
Db 301 TTCACGTTTCGGCTCGGGGACAAAAGTTGGAATAAAACG 338

RESULT 7
AR072863 339 bp DNA linear PAT 28-AUG-2000
LOCUS AR072863
DEFINITION Sequence 88 from patent US 5948658.
ACCESSION AR072863
VERSION AR072863.1 GI:9999626
KEYWORDS Location/Qualifiers
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 339)
AUTHORS Landry,D.W.
TITLE Anti-cocaine catalytic antibody
JOURNAL Patent: US 5948658-A 88 07-SEP-1999;
FEATURES Location/Qualifiers
source
1..339
/organism="unknown"
BASE COUNT 86 a 72 c 88 g 93 t
ORIGIN

Query Match 72.6%; Score 317.2; DB 6; Length 339;
Best Local Similarity 96.2%; Pred. No. 3.1e-93;
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTGATAAACCAGGATGAACCTCTCCAATCTGTCACTTCTGGAGAAATCAGTTTCC 155
Db 1 GATATTGTGATAAACCAGGATGAACCTCTCCAATCTGTCACTTCTGGAGAAATCAGTTTCC 60
QY 156 ATCTCCTCAGGTCTAGTAAGAGTCTCCTGTATAGGATGGGAACACATCTTGAATTGG 215
Db 61 ATCTCCTCAGGTCTAGTAAGAGTCTCCTGTATAGGATGGGAACACATCTTGAATTGG 120
QY 216 TTCTTCGAGAGACCAGGACAATCTCCTCAGCTCCTGTATTTGATGTCACCGGTGCA 275
Db 121 TTCTTCGAGAGACCAGGACAATCTCCTCAGCTCCTGTATTTGATGTCACCGGTGCA 180
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGCACAGATTTCCACCTGGAATC 335
Db 181 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGCACAGATTTCCACCTGGAATC 240
QY 336 AGTAGAGTCAAGGCTCAGGATGTTGGTGTATTACTGTCAACAATTTGTAGATATCCA 395
Db 241 AGTAGAGTCAAGGCTCAGGATGTTGGTGTATTACTGTCAACAATTTGTAGATATCCA 300

```



```
Db 241 AGTAGAGTGAAGGCTGAGGATGGGTGGTATTACTGTCAACAATTGTAGAGTATCCA 300
QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAATAAAGC 433
Db 301 TTCACGTTCCGGCTCGGGGACAAAGTTGGAATAAAGC 338

RESULT 11
AR166319          AR166319          420 bp      DNA          linear      PAT 17-OCT-2001
LOCUS             Sequence 111 from patent US 6280987.
DEFINITION
ACCESSION         AR166319
VERSION           AR166319.1 GI:16241586
KEYWORDS
SOURCE            Unknown.
ORGANISM          Unclassified.
REFERENCE         1 (bases 1 to 420)
AUTHORS           Landry,D.W.
TITLE             Anti-cocaine catalytic antibody
JOURNAL           Patent: US 6280987-A 111 28-AUG-2001;
FEATURES          Location/Qualifiers
SOURCE            1. 420
/organism="unknown"
BASE COUNT        98 a 95 c 115 g 108 t 4 others
ORIGIN

Query Match      72.3%; Score 316; DB 6; Length 420;
Best Local Similarity 95.6%; Pred. No. 7.9e-93;
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 94 GGGATATTGTGATAACCCAGGATGAACCTCCCAATCCTGTCACTCTCTGGAGAAATCAGTTT 153
Db 51 GCGATATGGTGATCACGACGAGTGAACCTCCCAATCCTGTCACTCTCTGGAGAAATCAGTTT 110
QY 154 CCATCTCCTCAGGCTCTAGTAAAGAGTCTCCTGTATAGAGTGGGAAGACATACTTGAATT 213
Db 111 CCATCTCCTCAGGCTCTAGTAAAGAGTCTCCTGTATAGAGTGGGAAGACATACTTGAATT 170
QY 214 GGTTCCTGCAGAGACCAAGGACAACTCTCCTCAGCTCCTGTATTTGATGTCCACCCGGTG 273
Db 171 GGTTCCTGCAGAGACCAAGGACAACTCTCCTCAGCTCCTGTATTTGATGTCCACCCGGTG 230
QY 274 CATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGCACAGATTTTCAACCTGGAAA 333
Db 231 CATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGCACAGATTTTCAACCTGGAAA 290
QY 334 TCAGTAGAGTGAAGGCTGAGAGTGGGTGTGTATTACTGTCAACAACCTGTAGAGTATC 393
Db 291 TCAGTAGAGTGAAGGCTGAGAGTGGGTGTGTATTACTGTCAACAACCTGTAGAGTATC 350
QY 394 CATTCACGTTCCGGCTCGGGGACAAAGTTGGAATAAAGC 433
Db 351 CATTCACGTTCCGGCTCGGGGACAAAGTTGGAATAAAGC 390

RESULT 12
AR072865          AR072865          368 bp      DNA          linear      PAT 28-AUG-2000
LOCUS             Sequence 90 from patent US 5948658.
DEFINITION
ACCESSION         AR072865
VERSION           AR072865.1 GI:9999628
KEYWORDS
SOURCE            Unknown.
ORGANISM          Unclassified.
REFERENCE         1 (bases 1 to 368)
AUTHORS           Landry,D.W.
TITLE             Anti-cocaine catalytic antibody
JOURNAL           Patent: US 5948658-A 90 07-SEP-1999;
FEATURES          Location/Qualifiers
SOURCE            1. 368
/organism="unknown"

BASE COUNT        95 a 80 c 93 g 100 t

Query Match      70.8%; Score 309.2; DB 6; Length 368;
Best Local Similarity 94.7%; Pred. No. 1.4e-90;
Matches 320; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 96 GATATTGTGATAACCCAGGATGAACCTCCCAATCCTGTCACTCTCTGGAGAAATCAGTTTCC 155
Db 1 GATATTGTGATGACGCAAGATGAACCTCCCAATCCTGTCACTCTCTGGAGAAATCAGTTTCC 60
QY 156 ATCTCCTCAGGCTCTAGTAAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 215
Db 61 ATCTCCTCAGGCTCTAGTAAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
QY 216 TTTCTGCAGAGACCAAGGACAACTCTCCTCAGCTCCTGTATTTGATGTCCACCCGGTGA 275
Db 121 TTTCTGCAGAGACCAAGGACAACTCTCCTCAGCTCCTGTATTTGATGTCCACCCGGTGA 180
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGCACAGATTTTCAACCTGGAATC 335
Db 181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGCACAGATTTTCAACCTGGAATC 240
QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCA 395
Db 301 TTTCAGTTTCGGCTCGGGGACAAAGTTGGAATAAAGC 338

RESULT 13
AR166315          AR166315          368 bp      DNA          linear      PAT 17-OCT-2001
LOCUS             Sequence 103 from patent US 6280987.
DEFINITION
ACCESSION         AR166315
VERSION           AR166315.1 GI:16241582
KEYWORDS
SOURCE            Unknown.
ORGANISM          Unclassified.
REFERENCE         1 (bases 1 to 368)
AUTHORS           Landry,D.W.
TITLE             Anti-cocaine catalytic antibody
JOURNAL           Patent: US 6280987-A 103 28-AUG-2001;
FEATURES          Location/Qualifiers
SOURCE            1. 368
/organism="unknown"

BASE COUNT        95 a 80 c 93 g 100 t
ORIGIN

Query Match      70.8%; Score 309.2; DB 6; Length 368;
Best Local Similarity 94.7%; Pred. No. 1.4e-90;
Matches 320; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 96 GATATTGTGATAACCCAGGATGAACCTCCCAATCCTGTCACTCTCTGGAGAAATCAGTTTCC 155
Db 1 GATATTGTGATGACGCAAGATGAACCTCCCAATCCTGTCACTCTCTGGAGAAATCAGTTTCC 60
QY 156 ATCTCCTCAGGCTCTAGTAAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 215
Db 61 ATCTCCTCAGGCTCTAGTAAAGAGTCTCCTGTATAAGGATGGGAAGACATACTTGAATTGG 120
QY 216 TTTCTGCAGAGACCAAGGACAACTCTCCTCAGCTCCTGTATTTGATGTCCACCCGGTGA 275
Db 121 TTTCTGCAGAGACCAAGGACAACTCTCCTCAGCTCCTGTATTTGATGTCCACCCGGTGA 180
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGCACAGATTTTCAACCTGGAATC 335
Db 181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGCACAGATTTTCAACCTGGAATC 240
QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCA 395
```

```

|||||
Db 241 AGTAGTGAAGGCTGAGGATGTGGTGTGTATTACTTTCAACACTTTGAAGACTATCCA 300
|||||
QY 396 TTCAGTTTCGCTCGGGACAAAGTTGGAATAAAACG 433
|||||
Db 301 TTCAGTTTCGCTCGGGACAAAGTTGGAATAAAACG 338
|||||

RESULT 14
MMIG28 825 bp DNA linear ROD 20-JUL-1995
LOCUS Mouse immunoglobulin variable gene V kappa-24 encoding amino acids
-4 to 95.
ACCESSION V00779
VERSION V00779.1 GI:51667
KEYWORDS germ line; Ig kappa light chain; immunoglobulin.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 825)
AUTHORS Gershenfeld,H.K., Tsukamoto,A., Weissman,I.L. and Joho,R.
TITLE Somatic diversification is required to generate the V kappa genes
of MOPC 511 and MOPC 167 myeloma proteins
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 78 (12), 7674-7678 (1981)
MEDLINE 82150933
PUBMED 6801657
FEATURES
    source          Location/Qualifiers
    1..825
        /organism="Mus musculus"
        /db_xref="taxon:10090"
    mRNA
    314..625
        /product="messenger RNA"
    CDS
    314..625
        /note="coding sequence; Protein sequence is in conflict
        with the conceptual translation"
        /codon_start=1
        /protein_id="CAA24156.1"
        /db_xref="GI:1333953"
        /translation="GVSGDIVITQDELSNPVTSGESVSIKRSKSLLYKDGKTVLNW
        FLORPGSQPLLIIYLMSTRASGVDRFSGSGTDTLEISRVAEDVGVYYCQQLVE
        YP"
BASE COUNT 248 a 147 c 198 g 232 t
ORIGIN

Query Match 70.5%; Score 308; DB 10; Length 825;
Best Local Similarity 98.4%; Pred. No. 3.6e-90;
Matches 311; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 79 TCCTCGAGTCAGTGGGATATTGTGATACCCAGGATGAATCTCCATCTGTGCACATT 138
|_|
Db 309 TTTCAGAGTCAGTGGGATATTGTGATACCCAGGATGAATCTCCATCTGTGCACATT 368
|||||
QY 139 CTGGAGAATCAGTTTCATCTCTCGAGGCTAGTAAGAGTCTCTCTGTATAAGGATGGGA 198
|||||
Db 369 CTGGAGAATCAGTTTCATCTCTCGAGGCTAGTAAGAGTCTCTCTGTATAAGGATGGGA 428
|||||
QY 199 AGACATCTGAATGGTTCTGCAGACACAGGACAATCTCCTCAGTCCTGTATGTATT 258
|||||
Db 429 AGACATCTGAATGGTTCTGCAGACACAGGACAATCTCCTCAGTCCTGTATGTATT 488
|||||
QY 259 TGATGTCCACCCCTGCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTCCAGGCACAG 318
|||||
Db 489 TGATGTCCACCCCTGCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTCCAGGCACAG 548
|||||
QY 319 ATTTACCCCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAAC 378
|||||
Db 549 ATTTACCCCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTCAAC 608
|||||
QY 379 AACTTGTAGATATCC 394
|||||
Db 609 AACTTGTAGATATCC 624
|||||

```

```

RESULT 15
MMU231264 899 bp DNA linear ROD 03-AUG-1999
LOCUS Mus musculus IgVκ hg24 gene.
ACCESSION AJ231264
VERSION AJ231264.1 GI:5305057
KEYWORDS IgVκ gene; immunoglobulin; kappa light chain; variable region.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 899)
AUTHORS Kirschbaum,T., Lamm,R., Ohnrich,M., Pourrajabi,S.,
Schaeble,K.F., Thiebe,R., Bensch,A., Brensing-Kueppers,J., Helm,V.,
Roeschenthaler,F., Schwendinger,J., Wichelhaus,D. and Zocher
Zachau,H.G.
TITLE Characteristics of the immunoglobulin Vκappa genes, pseudogenes,
relics and orphans in the mouse genome
JOURNAL Eur. J. Immunol. 29 (7), 2082-2086 (1999)
MEDLINE 99354924
PUBMED 10427970
REFERENCE 2 (bases 1 to 899)
AUTHORS Kirschbaum,T.
TITLE Direct Submission
JOURNAL Submitted (23-DEC-1998) T. Kirschbaum, Adolf-Butenandt-Institut
fuer, Physiologische Chemie, Schillerstr. 44, D-80336 Muenchen, FRG
FEATURES
    source          Location/Qualifiers
    1..899
        /organism="Mus musculus"
        /strain="C3H"
        /db_xref="taxon:10090"
        /chromosome="6"
        /clone="ICRFy90G0497"
        /sub_clone="cosmid T1"
        /haplotype="c"
        /tissue_type="spleen"
        /clone_lib="Reference library, ICRF"
        /gene="hg24"
        29..36
            /gene="hg24"
        /gene="hg24"
        /note="octamer regulatory sequence"
        102..107
            /gene="hg24"
            join(<135..183,549..>859)
        /gene="hg24"
        /codon_start=1
        /product="immunoglobulin light chain variable region"
        /protein_id="CAB46171.1"
        /db_xref="GI:5305058"
        /translation="MRCSLQFLGLVMFWISGVSDIVITQDELSNPVTSGESVSIKRS
        SKSLLYKDGKTVLNWFLORPGSQPLLIIYLMSTRASGVDRFSGSGTDTLEISR
        VKAEDVGVYYCQQLVEYP"
        join(<135..183,549..>859)
        /gene="hg24"
        /product="variable region of immunoglobulin kappa light
        chain"
        135..183
            /gene="hg24"
            number=1
        184..548
            /gene="hg24"
            number=1
        549..859
            /gene="hg24"
            number=2
        861..867
            /gene="hg24"
        /note="heptamer recombination signal"
        880..888
            /gene="hg24"
        /note="nonamer recombination signal"

```


Sat Apr 26 08:30:31 2003

```
BASE COUNT      249 a      183 c      203 g      264 t
ORIGIN
Query Match      70.5%; Score 308; DB 10; Length 899;
Best Local Similarity 98.4%; Pred. No. 3.6e-90;
Matches 311; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 79 TCTCTGGAGTCAGTGGGGATATTGTGATAACCCAGGATGAACCTCTCCAATCCTGTGCACATT 138
   |||||||
Db 543 TTTCCAGGAGTCAGTGGGGATATTGTGATAACCCAGGATGAACCTCTCCAATCCTGTGCACATT 602
   |||||||
QY 139 CTGGAGAAATCAGTTTCCATCTCCTGCAGGCTAGTAAGAGTCTCCTGTATAAGGATGGGA 198
   |||||||
Db 603 CTGGAGAAATCAGTTTCCATCTCCTGCAGGCTAGTAAGAGTCTCCTGTATAAGGATGGGA 662
   |||||||
QY 199 AGACATACCTTGAATTGGTTTCTGCAGAGACCAGGACAAATCTCCTCAGCTCCTGATGATT 258
   |||||||
Db 663 AGACATACCTTGAATTGGTTTCTGCAGAGACCAGGACAAATCTCCTCAGCTCCTGATGATT 722
   |||||||
QY 259 TGATGTCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGCACAG 318
   |||||||
Db 723 TGATGTCCACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGCACAG 782
   |||||||
QY 319 ATTTCCACCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTATTACTGTCAAC 378
   |||||||
Db 783 ATTTCCACCTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTATTACTGTCAAC 842
   |||||||
QY 379 AACTTGTAGAGTATCC 394
   |||||||
Db 843 AACTTGTAGAGTATCC 858
```

Search completed: April 26, 2003, 06:31:03
Job time : 875.354 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:55:21 ; Search time 578.185 seconds
(without alignments)
12240.775 Million cell updates/sec

Title: US-09-674-716B-2

Perfect score: 437

Sequence: 1 aagctttacattactcagc.....agttggaataaaacgtacg 437

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	318.8	73.0	343	12	BF023001
2	311.4	71.3	351	10	BF870732
3	290	66.4	906	12	BF785914
4	281.2	64.3	400	10	AW912881
5	280	64.1	935	11	BC031349
6	256	58.6	725	13	BG963055

7	253.4	58.0	634	14	BM783161
8	251.8	57.6	522	13	BM511309
9	250.2	57.3	751	12	BG542438
10	250.2	57.3	787	12	RG536224
11	250	57.2	995	14	BQ712430
12	249.2	57.0	491	12	BF174573
13	248.6	56.9	425	9	AI734035
14	248.6	56.9	442	9	AA405415
15	248.6	56.9	880	12	BG755003
16	248.6	56.9	880	12	BG755003
17	247.2	56.6	410	12	BG059215
18	246.2	56.3	382	9	AI882479
19	245.4	56.2	643	14	BM820052
20	244	55.8	488	14	H25625
21	243.8	55.8	926	12	BG342051
22	243	55.6	960	14	BQ711007
23	240.8	55.1	359	10	BB870575
24	240.8	55.1	770	12	BG530186
25	240.8	55.1	990	13	BI838327
26	240.6	55.1	701	12	BG547597
27	240.6	55.1	774	13	BM007808
28	239.8	54.9	427	12	BF174767
29	238.4	54.6	614	10	AW405187
30	237.4	54.3	462	12	BF176195
31	237.4	54.3	898	14	BQ708918
32	235.6	53.9	485	12	BF174421
33	234.8	53.7	424	12	BF176198
34	234.8	53.7	958	14	BQ709417
35	234.2	53.6	597	12	BF868788
36	234.2	53.6	650	13	BI765629
37	233.8	53.5	952	12	BG758592
38	233.4	53.4	816	13	BI759427
39	232.6	53.2	816	13	BI759427
40	232.6	53.2	908	12	BG685179
41	231.8	53.0	783	12	BG541344
42	231.2	52.9	421	14	BM894491
43	231.2	52.9	421	14	BQ130227
44	231.2	52.9	421	14	BQ267173
45	231.2	52.9	421	14	BQ267663

ALIGNMENTS

RESULT 1
BF023001
LOCUS
DEFINITION
ux02c02.yl Soares_thymus_2ndmt Mus musculus cdna clone
IMAGE:3470306 5' similar to SW:KV2B_MOUSE P01627 IG KAPPA CHAIN
V-II REGION VKAPPA167 PRECURSOR. ;, mRNA sequence.
343 bp mRNA linear EST 10-OCT-2000
BF023001
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 343)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1389666
Trace considered overall poor quality
Seq primer: -40RP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
I. .343
/organism="Mus musculus"

```

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3470306"
/clone_lib="Soares_thymus_2NDMT"
/sex="male"
/tissue_type="thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notes: Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTCACCATCTGAGTGGGAGCGCCGGTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT      89 a   72 c   86 g   96 t
ORIGIN
Query Match      73.0%; Score 318.8; DB 12; Length 343;
Best Local Similarity 97.9%; Pred. No. 1.4e-86;
Matches 323; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 65 GCTTATGTTCTGGATCTCTGGAGTCAGTGGGATATTGTGATAACCCAGGATGAATCTTC 124
DB 13 GCTTATGTTCTGGATCTCTGGAGTCAGTGGGATATTGTGATAACCCAGGATGAATCTTC 72

QY 125 CAATCCGTGTCATCTCTGGAGAATCAGTTCCTCCATCTCTGCAGGTCCTAGTAAGAGTCTCCT 184
DB 73 CAATCCGTGTCATCTCTGGAGAATCAGTTCCTCCATCTCTGCAGGTCCTAGTAAGAGTCTCCT 132

QY 185 GTATAAGGATGGGAAGACATACCTGAATGGTTTCTGCAGAGACCCAGGACAATCTCTCTCA 244
DB 133 ATATAAGGATGGGAAGACATACCTGAATGGTTTCTGCAGAGACCCAGGACAATCTCTCTCA 192

QY 245 GCTCCTGATGTTATGATGTCACCGTGCATCAGGAGTCTCAGACCGGTTAGTGGGAG 304
DB 193 GCTCCTGATGTTATGATGTCACCGTGCATCAGGAGTCTCAGACCGGTTAGTGGGAG 252

QY 305 TGGGTGAGGCACAGATTTCACCTCGGAAATCAGTAGAGTGAAGGCTGAGGAGTGTGGGTGT 364
DB 253 TGGGTGAGGCACAGATTTCACCTCGGAAATCAGTAGAGTGAAGGCTGAGGAGTGTGGGTGT 312

QY 365 GTATTACTGTCAACAACCTGTGAGATATCC 394
DB 313 GTATTACTGTCAACAACCTGTGAGATATCC 342

```

```

RESULT 2
BB870732      351 bp  mRNA  linear  EST 27-NOV-2001
LOCUS      BB870732 RIKEN full-length enriched, adult male jejunal and colic
DEFINITION  lymph node Mus musculus cDNA clone G630024M15 5', mRNA sequence.
ACCESSION  BB870732
VERSION    BB870732.1 GI:17116942
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 351)
REFERENCE  Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
AUTHORS    Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
            Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Konda,M., Matsuyama,T.,
            Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
            Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
            Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,
            A., Takahashi,F., Takaku-Akashira,S., Tanaka,T., Tomaru,A., Toyota,
            Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
            RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
            2001)
TITLE

```

JOURNAL COMMENT

Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-res@genome.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuda
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

e mouse tissues.

Location/Qualifiers

```

1. 351
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G630024M15"
/clone_lib="RIKEN full-length enriched, adult male jejunal
and colic lymph node"
/sex="male"
/tissue_type="jejunal and colic lymph node"
/dev_stage="adult"
/notes="pooled tissues : (tissue_type=cerebellum,
dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=males), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed)"

```

```

BASE COUNT      89 a   77 c   87 g   98 t
ORIGIN

```

```

Query Match      71.3%; Score 311.4; DB 10; Length 351;
Best Local Similarity 96.7%; Pred. No. 2.6e-84;
Matches 318; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```

```

QY 24 CAGGACCTCACCATGAGGTTCTCTGTTCAAGTTCTGGGGGTGCTTATGTTCTGGATCTCT 83
DB 23 CAAGTTCTCAGAATGAGGTGCTCTCTTCAGTTCCTGGGGGTGCTTATGTTCTGGATCTCT 82

QY 84 GGAGTCAGTGGGGATATTGTGATAACCCAGGATGAACCTCTCAATCTCTGTCACCTCTGGA 143
DB 83 GGAGTCAGTGGGGATATTGTGATAACCCAGGATGAACCTCTCAATCTCTGTCACCTCTGGA 142

QY 144 GAATCAGTTTCCATCTCTCTCGAGGTCCTAGTAAGAGTCTCCCTGTTATAGGATGGGAAGACA 203
DB 143 GAATCAGTTTCCATCTCTCGAGGTCCTAGTAAGAGTCTCCCTGTTATAGGATGGGAAGACA 202

QY 204 TACTTGAATGGTTTCTTCAGACAGGACCAATCTCTCAGCTCCTTCATGTTATTTGATG 263
DB 203 TACTTGAATGGTTTCTTCAGACAGGACCAATCTCTCAGCTCCTTCATGTTATTTGATG 262

QY 264 TCCACCCCTGGATCAGGAGTCTCAGACCGGTTTASTGSCAGTGGGTGAGGCACACGATTTTC 323

```

```
Db 263 TCACCCGTCATCAGGAGTCTCAGACCGGTTTATTGGCAGTGGGTGAGAACAGATTTC 322
QY 324 ACCCTGGAATCAGTAGAGTGAAGCTGA 352
Db 323 ACCCTGGAATCAGTAGAGTGAAGCTGA 351

RESULT 3
BF785914
LOCUS BF785914
DEFINITION 602112548F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4240762
5', mRNA sequence.
ACCESSION BF785914
VERSION BF785914.1 GI:12090950
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9855 row: p column: 11
High quality sequence stop: 718.
FEATURES
source
1..906
Location/Qualifiers
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4240762"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
Note=Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: This is a NCI_CGAP Library. |"
BASE COUNT 243 a 232 c 237 g 194 t
ORIGIN
Query Match 66.4%; Score 290; DB 12; Length 906;
Best Local Similarity 81.7%; Pred. No. 1.3e-77;
Matches 335; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 24 CAGGACCTCACCATGAGGTTCTCTTTCAGTTTCGGGGTGCCTTATGTTCTGGATCTCT 83
Db 3 CAAAGTTCTCAGATGAGGTCCTTAGCTGATGTTCCCTGGGGCTGCTGTGCTCTGGATCCT 62
QY 84 GGAGTCAGTGGGGATATTGTGATAACCCAGGATGAACCTCCCAATCTCTCACTCTCTGGA 143
Db 63 GGAGCATTTGGGATATTCTGATGACTCAGGCTGTACCCCTCTGACTGTCACTCTCTGGA 122
QY 144 GAATCAGTTTCCATCTCTGCAAGGTCCTAGTAAGAGTCTCTCTGTATAAGGATGGGAAGACA 203
Db 123 GAGTCAGTATCCATCTCTCTGCAGGCTCTAGTAAGAGTCTCTTTCATAGTATGATGGCTACACT 182
QY 204 TACTTCAATTGGTTCTGAGAGACCCAGGACAACTCTCTCAGCTCCTGATGATTGATG 263
Db 183 GACTTGTATGGTTCTACAGAGGCCAGGCCAGCTCTCTCAGCTCCTGATATATCGGATG 242
QY 264 TCACCCGTCATCAGGAGTCTCAGACCGGTTTATTGGCAGTGGGTGAGGACACAGATTTC 323
Db 243 TCCACCTTGCTCAGGAGTCCAGACAGGTTTCAGTGGCAGTGGGTGAGGAACTGCTTTC 302
```

```
QY 324 ACCCTGGAATCAGTAGAGTGAAGCTCAGGATGTGGTGTGTTATTACTCTCAACACTT 383
Db 303 ACACAGGAATCAGTAGAGTGAAGCTCAGGATGTGGTGTGTTATTACTCTTTCGAACAT 362
QY 384 GTAGAGTATCCATTACAGTTTCGGCTCGGGGACAAAGTTGGAATAAAACG 433
Db 363 CTAGAATATCGTACACGTTCTGGAGGGGGGACCAAGCTGGAATAAAACG 412

RESULT 4
AW912881
LOCUS AW912881
DEFINITION uf46b05.y1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
IMAGE:1514385 5' similar to gb:J00560 mouse ig kappa mRNA from
mopc21 & other myeloma mRNA 3' (MOUSE);, mRNA sequence.
ACCESSION AW912881
VERSION AW912881.1 GI:8078508
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:941237
Seq primer: -40RP from Gibco.
FEATURES
source
1..400
Location/Qualifiers
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1514385"
/clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
Note=Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Ronaldo.
BASE COUNT 90 a 90 c 110 g 110 t
ORIGIN
Query Match 64.3%; Score 281.2; DB 10; Length 400;
Best Local Similarity 81.7%; Pred. No. 4.7e-75;
Matches 325; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTCAGTTTCGGGGTGCCTTATGTTCTGGATCTCTCGAGTCAGTGG 95
Db 2 ATTCGGTAGAGGCTGTTTTCGGGGTGCCTTGTGCTCTGGATCCTCGAGGCAATGGG 61
QY 96 GATATTGTGATACCCAGGATGAACCTCCCAATCTCTCACTCTCTGGAGATCAGTTTCC 155
Db 62 GATATTGTGATGACTCAGGCTGCACCCCTCTCTACTCTCTCGAGATCAGTATCC 121
QY 156 ATCTCTCGAGGCTAGTAGAGTCTCTCTGTATAAGGATGGGAGACATCTACTGAATGG 215
Db 122 ATCTCTCGAGGCTAGTAAAAGTCTCTGATATTGATGCAACACTTATTTATATGG 181
QY 216 TTTCTGAGAGACACAGGACAACTCTCTCAGCTCTCTGATGATTGATGTCACCCGTCGA 275
Db 182 TTCTGCGAGAGGCCAGGCCAGTCTCTCAGCTCTGATATATCGGATGTCACACCTTGTG 241
```

Qy	276	TCAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGGTGTCAGGCACAGATTTCACCCCTGGAATC	335
Db	242	TCAGAGTCCACAGACAGGTTTCAGTGGCAGTGGGTTCAGGAACCTGCTTTCACACTGAGAATC	301
Qy	336	AGTAGTGAAGGCTGAGGATGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCA	395
Db	302	AGTAGTGAAGGCTGAGGATGGGTGTGTATTACTGTCAACAACCTGTAGAGTATCCA	361
Qy	396	TTCAGTTCGCGCTCGGGGCAACAAGTTGGAATAAAACG	433
Db	362	TACAGTTCGGAGGGGGACCAAGCTGGAATAAAACG	399

BC031349 935 bp mRNA linear HTC 03-JUN-2002

LOCUS BC031349 Mus musculus, clone IMAGE:1514385, mRNA.

ACCESSION BC031349

VERSION BC031349.1 GI:21315064

KEYWORDS HTC.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 935)

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (03-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NTH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
cDNA Library Preparation: Soares Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 67 Row: j Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
This clone has the following problem: no cloning site / microdeletion.

FEATURES
source Location/Qualifiers
1..935
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1514385"
/tissue_type="Mammary gland, lactating mouse"
/clone_lib="Soares_mammary_gland_NMLMG"
/lab_host="DH10B"
/note="Vector: pT73D-Pac"
BASE COUNT 251 a 247 c 208 g 229 t
ORIGIN

Query Match 64.1%; Score 280; DB 11; Length 935;
Best Local Similarity 83.1%; Pred. No. 1.5e-74;
Matches 319; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy	50	TCAGTTTCTGGGGTGCTTATGTTCTGGATCTCTGGAGTCTAGTGGGATATTGTGATAAC	109
Db	2	TCAGTTTCTGGGGTGCTTATGTTCTGGATCTCTGGAGTCTAGTGGGATATTGTGATAAC	61
Qy	110	CCAGGATGAACCTCTCAATCCCTGTCACATCTCTCGAGAACATGTTCCATCTCCTCGAGGTC	169
Db	62	TCAGGCTGCACCCCTCTGTACCTGTCTCTCGAGAGTCAGTATCCATCTCCTCGAGGTC	121
Qy	170	TAGTAAGAGTCTCCCTGTATAAGGATGGGAAGACATATTGAATTGGTTTCTTCGACAGACC	229
Db	122	TAGTAAAGTCTCCCTGCATATTGATGGCAACACTATTATTATTTGTTCTTCGACAGGCC	181
Qy	230	AGGACAATCTCTCAGCTCTCATGTTATTTGATGTCCACCCCTGCAATCAGGAGTCTCAGA	289
Db	182	AGGCCAGTCTCTCAGCTCTCATGTTATTTGATGTCCACCCCTGCAATCAGGAGTCTCAGA	241
Qy	290	CCGGTTTACTGTCAGTGGGTGAGGCACAGATTTCCACCTGGAAATCAGTAGAGTCAAGGC	349
Db	242	CAGGTTTCAGTGGCAGTGGGTGAGGCACAGATTTCCACCTGGAAATCAGTAGAGTCAAGGC	301
Qy	350	TGAGGATGGGTGTATTACTGTCAACACTTTAGAGTATCCATTACGTTTCGGGCTC	409
Db	302	TGAGGATGGGTGTATTACTGTCAACACTTTAGAGTATCCATTACGTTTCGGGCTC	361
Qy	410	GGGGACAAGTTGGAAATAAAACG	433
Db	362	GGGGACAAGTTGGAAATAAAACG	385

RESULT 6

LOCUS BG963055 725 bp mRNA linear EST 12-JUN-2001

DEFINITION 602828068F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982825 5', mRNA sequence.

ACCESSION BG963055

VERSION BG963055.1 GI:14350692

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 725)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM10986 row: g column: 18
High quality sequence stop: 719.

FEATURES
source Location/Qualifiers
1..725
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4982825"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1; Notf; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 195 a 182 c 174 g 174 t
ORIGIN

Query Match 58.6%; Score 256; DB 13; Length 725;
Best Local Similarity 79.8%; Pred. No. 3e-67;

RESULT 10
BG536224


```

LOCUS       BG536224               787 bp    mRNA    linear    EST 03-APR-2001
DEFINITION  602565445F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4690258 5',
            mRNA sequence.
ACCESSION   BG536224
VERSION     BG536224.1 GI:13527769
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 787)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCMI507 row: i column: 11
            High quality sequence stop: 721.
            Location/Qualifiers
                1..787
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:4690258"
                /clone_lib="NIH_MGC_77"
                /lab_host="DH10B (T1 phage-resistant)"
                /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                SfiI (ggccgctcgccc); Site_2: SfiI (ggccattatggcc); 5' and
                3' adaptors were used in cloning as follows: 5' adaptor
                sequence: 5'-CACGGCATATGGCC-3' and 3' adaptor sequence:
                5'-ATTAGAGCGGAGGGCGGCACATG-dt(30)BN-3' (where B = A,
                C, or G and N = A, C, G, or T). Average insert size 1.9
                kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                by PCR. This library was enriched for full-length clones
                and was constructed by Clontech Laboratories (Palo Alto,
                CA). Note: this is a NIH_MGC Library."
BASE COUNT  196 a 213 c 188 g 190 t
ORIGIN
Query Match 57.3%; Score 250.2; DB 12; Length 787;
Best Local Similarity 75.9%; Pred. No. 1.8e-65;
Matches 309; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 30 CTCACCATGAGTTCTCTGTTTCAGTTTCTGGGGGTGCTTATGTTCTGGATCTCTGGAGTC 89
    ||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 26 CTCACAATGAGGTCCTCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGGTCTCTGGATCC 85
    ||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||

QY 90 AGTGGGATATTGTGATACCCAGATGAACCTCTCCATCTCTGTCACCTTCACCTTCGGAGAATCA 149
    ||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
DB 86 AGTGGGATATTGTGATGACTACTCAGTCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCG 145
    ||||| ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||

QY 150 GTTTCATCTCTCGAGGCTAGTAGAGTCTCTGTATAGGATGGAAGACATACTTG 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 146 GCCTCATCTCTGCAAGGCTAGTCAGACCCCTCTGCAATAGTAATGGAACAACATATTG 205
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 210 AATTGGTTTCTGAGACAGCAGGACAATCTCTCAGCTCTCTGATGATATTGATGCCACC 269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 206 GATTGTACTGCAAGACCGAGGAGCTCTCCACAGCTCTCTGATCTATTGGGTTCTAAT 265
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 270 CGTGCAATCAGGAGCTTCAGACCGGTTTGTAGTGGCAGTGGGTAGGACACAGATTTCACCTG 329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 266 CGGGCTCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATGAGGACAGATTTCACCTG 325
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 330 GAATCAGTAGAGTGAAGCTGAGGATGTGGGTGCTGTTACTTACTGTCAACAACCTTGTAGAG 389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 326 AAAATCAGTAGAGTGAGGCTGAGGATGTGGGGTTTATTACTGCAATGCAAGCTCTACAA 385
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

QY 390 TATCCATTACGTTCCGCTCGGGGACAAAGTTTGGAAATAAATAACGTAC 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 386 ACTCTAGGACCTTCGCCCAAGGACACGACTGGAGATTAAACGAAC 432
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
LOCUS      B0712430
DEFINITION AGENCOURT_8352203 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277729
            5' mRNA sequence.
ACCESSION   B0712430
VERSION     B0712430.1 GI:21851329
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 995)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue Procurement: Dr. Mark Watson
            cDNA Library Preparation: Rubin Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2464 row: j column: 02
            High quality sequence stop: 645.
            Location/Qualifiers
                1..995
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:6277729"
                /clone_lib="NIH_MGC_113"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCACGAG(G). Library constructed by Ling Hong in the
                laboratory of Gerald M. Rubin (University of California,
                Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                Superscript II RT (Life Technologies). Note: this is a
                NIH_MGC Library."
BASE COUNT  242 a 273 c 252 g 227 t 1 others
ORIGIN
Query Match 57.2%; Score 250; DB 14; Length 995;
Best Local Similarity 76.4%; Pred. No. 2.3e-65;
Matches 307; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 35 CATCAGGTTCTCTGTTTCAGTTTCTGGGGTGCCTATGTTCTGGATCTCTGAGTCAGTGG 94
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 6 CATCAGGTCCTCTGCTCAGTCTCGGGGCTGCTAATGCTCTGGGTCTCTGGATCCAGTGG 65
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 95 GGATATTGTGATAACCCAGGATGAACCTCTCAATCTCTGTCACCTCTCGAGAATCAGTTTC 154
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 66 GGATATTGTGATGACTCAGTCTCCACCTCTCCCTGCCGTCACCCCTCGAGAGCGGCTC 125
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 155 CATCTCTCGAGGCTAGTAAGAGTCTCCTGTATAGAGATGGGAAGACATACTTTGAATTG 214
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 126 CATCTCTCGAGGCTAGTCAGAGCCTCTGCATAGTAATGATGATCAACTATTATAGATTG 185
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 215 GTTTCGACAGACCCAGGACAATCTCTCAGCTCTCTGATGATTTATGATGCCACCCCTGC 274
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 186 GTACTCTGCAAGAGCAGGGCAGTCTCCACAGCTCTCCATCTATTATTTGGGTTCTAATCGGGC 245
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 275 ATCAGGAGCTCTCAGACCGGTTTGTAGTGGCAGTGGGTGAGGATGAGGATGAGGATGAGGAT 334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 246 CTCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGGATGAGGATGAGGATGAGGATGAGGAT 305
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Qy	30	CTCACCATTAGGTTCTCTGTTTCAGTTTCTCTGGGGTGGCTTATGTTCTGTGATCTCTGGAGTC	89
Db	15	CTCACATGAGGCTCCCTGCTCAGCTCTCTGGGGTCTCTAATGCTCTGGGTCTCTGGATCC	74
Qy	90	AGTGGGGATATTGTGATAACCCAGGATGAACCTCTCCAATCTCTGCATCTCTGGAGATCA	149
Db	75	AGTGGGGATATTGTGATGACTCAGTCTCCACATCTCCCTGCCGTCACCCCTGGAGAGCCG	134
Qy	150	GTTCCTCATCTCCTGCAGGCTAGTAGAGTCTCCCTGTATATAGGATGGGAGACATACTTG	209
Db	135	GCCTCATCTCTCTGCAGGCTAGTCAGAGCCCTGTCATGATATGGATGATACAACTATTG	194
Qy	210	AATTGGTTTCTGCAGAACCCAGGACAATCTCTCAGCTCTCTGCATGTATTTGATCTCCACC	269
Db	195	GATTGGTACCTGCAGAAAGCCAGGCAGTCTCCACAGCTCTGATCTATTTGGGTCTTAAT	254
Qy	270	CGTGCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGCAGATTTCCACCTG	329
Db	255	CGGGCTTCGGGNCCTCCAGAGGTTCACTGGCAGTGGATCAGCAGACAGATTTTACACTG	314
Qy	330	GAATCAGTAGAGTGAAGGCTCAGGATGTGGGTGTGTATTACTGTCAACAACCTGTGTAGAG	389
Db	315	AAATCAGCAGAGTGGAGGCTCAGGATGTGGGTATTTACTGCATGCAAGCTCTACAA	374
Qy	390	TATCCATTACGTTCCGCTCGGGACAAGTTGGNAATAAAACGTAC	436
Db	375	ACTCTCAGACTTTTGGCCAGGGGACCAAGCTGGAGATCAAAACGAAC	421
RESULT	13		
LOCUS	AI734035		
DEFINITION	zu56d02.y5 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:741987 5', similar to gb:X72467 IG KAPPA CHAIN PRECURSOR V-II REGION (HUMAN);, mRNA sequence.		
ACCESSION	AI734035		
VERSION	AI734035.1	GI:50551148	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 425)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997) Other_ESTS: zu56d02.s1 Contact: Robert Strausberg, Ph.D. This clone is available royalty-free through LLNL: contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESQUENCE of a previously sequenced human clone Original clone citation: WashU-NCI human EST Project This read has been verified (found to hit its original self in the correct orientation) Insert Length: 1053 Std Error: 0.00 Seq primer: -408p from Gibco.		
FEATURES	Location/Qualifiers		
source	1..425		
	/organism="Homo sapiens"		
	/db_xref="GDB:5942254"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:741987"		
	/clone_lib="Soares ovary tumor NBH07"		
	/sex="Female"		
	/tissue_type="ovarian tumor"		
	/lab_host="DH10B (ampicillin resistant)"		
	/note="Organ: ovary; Vector: p77T3D (Pharmacia) with a modified polylinker; Site.1: Not 1; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATCTGAAGTGGAGCGCGCGGTGTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI		

adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

```

BASE COUNT      88 a 114 c 111 g 112 t
ORIGIN

Query Match      56.9%; Score 248.6; DB 9; Length 425;
Best Local Similarity 75.7%; Pred. No. 4.4e-65;
Matches 308; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 30 CTCACCATGAGTTCTCTGTTTCAGTTCTGGGGGCTTATGTTCTGGATCTCTGGAGTC 89
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 15 CTCACAATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGTCTCTGGATCC 74
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 90 AGTGGGGATATTGCTATACCCAGGATGAATCTCCATCTCCTGTCACATCTCTGGAGAATCA 149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 75 AGTGGGGATATTGCTATACCCAGGATGAATCTCCATCTCCTGTCACATCTCTGGAGAGCCG 134
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 150 GTTTCATCTCTCGAGGCTAGTAGAGTCTCTGTTATAGGATGGGAAGACATACCTTG 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 135 GCCTCCATCTCTGCAAGTCTAGTCAGAGCCTCCTGCTTAGTAAATGATATAATTATTG 194
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 210 AATTGGTTTCTGAGAGACAGGACAATCTCTCAGCTCCTGATGATATTGATGTCACC 269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 195 GATTGGTATCTGCAGAAGCAGGCGAGTCTCCACAGCTCCTGATCTATTTTGGGTTCTAAT 254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 270 CGTGATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGTGTATTAAGTCAACAACCTGAGAG 329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 315 AAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATCACTGCATGAGGCTCTACAA 374
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 330 GAAATCAGTAGAGTGAAGGCTGAGGATGTTGGGTGTGTATTACTCAACAACCTGTAGAG 389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 315 AAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATCACTGCATGAGGCTCTACAA 374
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 390 TATCCATTACGTTTCGGCTCGGGGACAAAGTTGGAATAAAACGTAC 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 375 TCTCCTCACACTTTTGGCCAGGGGACCAAGCTGGAGATCAACAGAAC 421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
AA05415      442 bp mRNA linear EST 09-NOV-1997
LOCUS      zu56d02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
DEFINITION IMAGE:741987 5' similar to gb:X72467 IG KAPPA CHAIN PRECURSOR V-II
REGION (HUMAN);, mRNA sequence.
ACCESSION  AA05415
VERSION     AA05415.1 GI:2063652
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 442)
AUTHORS    Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krieman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE       WashU-NCI human EST Project
JOURNAL     Unpublished (1997)
COMMENT     Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1053 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham.
FEATURES
source      Location/Qualifiers
            1..442
            /organism="Homo sapiens"

```

```

/db_xref="GDB:5942254"
/db_xref="taxon:9606"
/clone="IMAGE:741987"
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: ovary; Vector: pT73D (Pharmacia) with a
modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT      90 a 120 c 114 g 118 t
ORIGIN

Query Match      56.9%; Score 248.6; DB 9; Length 442;
Best Local Similarity 75.7%; Pred. No. 4.5e-65;
Matches 308; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 30 CTCACCATGAGTTCTCTGTTTCAGTTCTGGGGGCTTATGTTCTGGATCTCTGGAGTC 89
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 15 CTCACAATGAGGCTCCCTGCTCAGCTCCTGGGGCTGCTAATGCTCTGGTCTCTGGATCC 74
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 90 AGTGGGATATTGTAACCCAGGATGAATCTCCCAATCTCTGTCACATCTCTGGAGAATCA 149
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 75 AGTGGGATATTGTAAGTACTAGTCTCCACTCTCCCTGCCCGTCATCCCTGGAGAGCCG 134
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 150 GTTTCATCTCTCGAGGCTAGTAGAGTCTCTGTTATAGGATGGGAAGACATACCTTG 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 135 GCCTCCATCTCTGCAAGTCTAGTCAGAGCCTCCTGCTTAGTAAATGATATAATTATTG 194
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 210 AATTGGTTTCTGAGAGACAGGACAATCTCTCAGCTCCTGATGATATTGATGTCACC 269
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 195 GATTGGTATCTGCAGAAGCAGGCGAGTCTCCACAGCTCCTGATCTATTTTGGGTTCTAAT 254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 270 CGTGATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGTGTATTAAGTCAACAACCTGAGAG 329
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 255 CGGGCTCCGGGTCCTGACAGCTTCAAGTTCAGTGGCAGTGGATCAGGACAGATTTTACACTG 314
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 330 GAAATCAGTAGAGTGAAGGCTGAGGATGTTGGGTGTGTATTACTCAACAACCTGTAGAG 389
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 315 AAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATCACTGCATGAGGCTCTACAA 374
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 390 TATCCATTACGTTTCGGCTCGGGGACAAAGTTGGAATAAAACGTAC 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 375 TCTCCTCACACTTTTGGCCAGGGGACCAAGCTGGAGATCAACAGAAC 421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
EG755003      880 bp mRNA linear EST 15-MAY-2001
LOCUS      602711509f1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851723 5',
DEFINITION mRNA sequence.
ACCESSION  EG755003
VERSION     EG755003.1 GI:14065656
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 880)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.N.A.G.E. Consortium (LLNL)

```

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCMI695 row: a column: 04
High quality sequence stop: 845.
Location/Qualifiers
1. .880
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4851723"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pOB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

BASE COUNT 204 a 266 c 216 g 194 t
ORIGIN
Query Match 56.9%; Score 248.6; DB 12; Length 880;
Best Local Similarity 75.7%; Pred. No. 5.9e-65;
Matches 308; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 30 CTCACCATGAGTCTCTGTTCAGTTTCTGGGGTGGTTATGTTCTGATCTCTGGAGTC 89
Db ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 5 CTCACAATGAGGCTCCTGCTCAGCTCTGGGGTGGTAAATGCTGTGGGCTCTGGATCC 64
QY 90 AGTGGGATATTGTATACCCAGGATGAATCTCTCCAAATCTGTCACTTCTGGAGATCA 149
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 65 AGTGGGAATTTGTGATGACTAGCTCTCCACTCTCCCTGCCCGTCACTCCCTGGAGCCG 124
QY 150 GTTTCATCTCCAGAGTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACATCTTG 209
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 125 GCCTCCATCTCCTGAGGTCTAGTCAGAGCTCTGTCAGAGCTCTGTCATAGCAATGGATACACCTATTG 184
QY 210 AATTGGTTTCTGCAGACCCAGGACAATCTCTCAGCTCCTGATGATTTGATGTCAC 269
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 185 GATTGGTACCTGCAGAGCCGGGCGAGTCTCCACAATCTCTGATCTATTGGGTCTAAT 244
QY 270 CGTGCATCAGAGTCTCAGACCGGTTTGTAGTGGAGTGGGTGAGGCACAGATTTACCCCTG 329
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 245 CGGCGCTCCGGGTCCCTGACAGGTTCAAGTGGCAGTGGATCAGGCACAGATTTTACACTG 304
QY 330 GAATCAGTAGAGTGAAGGCTGAGGATGTTGGTGTGTATTACTGTCAACAACCTTTAGAG 389
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 305 AAGATCAACAGATGGAGGCTGAGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAA 364
QY 390 TATCCATTACGTTCCGCTCGGGACAAAGTTGGGAATAAAGCTAC 436
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
QY 365 ACTCCCTTCACTTCGGCCCTGGGACCAAGTGGAAATCAACAGAC 411

Search completed: April 26, 2003, 07:26:43
Job time : 585.185 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:50:01 ; Search time 87.9172 Seconds
(without alignments)
11193.756 Million cell updates/sec

Title: US-09-674-716B-2

Perfect score: 437

Sequence: 1 aagctttacagttactcagc.....agttggaaataaacgtacg 437

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	437	100.0	437	21	AAZ34746 Mouse anti-CD23 MA
2	366.4	83.8	429	12	AAQ12056 Sequence encoding
3	366.4	83.8	429	12	AAQ12012 Sequence encoding
4	317.2	72.6	340	19	AAV09791 DNA encoding the 1
5	317.2	72.6	368	19	AAV09789 DNA encoding the 1
6	316	72.3	420	19	AAV09802 DNA encoding the 1
7	309.2	70.8	368	19	AAV09793 DNA encoding the 1
8	293.2	67.1	464	14	C242:11 MAB kappa
9	293.2	67.1	464	14	AAQ36950 C242 kappa chain v

10	286.8	65.6	961	16	AAQ79929 Anti-tobacco mosai
11	277.2	63.4	441	11	AAQ08602 B38.1 Light Chain
12	277.2	63.4	441	18	AAV74344 MAB B38-1 light ch
13	277.2	63.4	441	20	AAV71152 Coding strand for
14	276.4	63.2	399	14	AAQ38878 CTMO1 VL cDNA. Sy
15	276.4	63.2	399	18	AAQ38878 Anti-HMFG MAB CTMO
16	276.4	63.2	399	21	AAZ46913 MAB CT-M-01 light
17	271.4	62.1	720	21	ABK10999 DNA encoding prote
18	257.2	58.9	348	21	AAZ34747 Humanised anti-CD2
19	255.6	58.5	720	21	AAAL3924 Human PTHR monocl
20	255	58.4	772	20	AAZ24418 Human bladder tumo
21	254.6	58.3	720	21	AAAL3927 Human PTHR monocl
22	253	57.9	720	21	AAAL3926 Human PTHR monocl
23	252.2	57.7	720	21	AAAL3925 Human PTHR monocl
24	251.8	57.6	720	21	AAAL3928 Human PTHR monocl
25	251.6	57.6	651	20	AAZ24421 Human bladder tumo
26	251.2	57.5	720	21	AAAL3920 Human PTHR monocl
27	251	57.4	793	24	ABK43188 DNA encoding const
28	250.8	57.4	720	21	AAAL3922 Human PTHR monocl
29	250.8	57.4	720	21	AAAL3923 Human PTHR monocl
30	250	57.2	501	20	AAZ57787 Anti-HCV Ser/Thr p
31	250	57.2	1111	24	ABK43191 DNA encoding fiber
32	250	57.2	1402	24	ABK43192 DNA encoding fiber
33	249.6	57.1	336	21	AAA38897 2G3 hybridoma VL d
34	249.4	57.1	963	22	AAF44895 Human breast cance
35	249	57.0	720	21	AAAL3921 Human PTHR monocl
36	248.4	56.8	339	21	AAA09017 Murine 13H10 light
37	243.4	55.7	373	19	AAV18472 TAL antibody VL ch
38	242.4	55.5	720	21	AAAL3929 Human PTHR monocl
39	238.4	54.6	882	15	AAQ73406 81C6 light chain v
40	236.2	54.1	417	22	AAH41159 Human coding seque
41	234.2	53.6	891	19	AAV66632 Human immunoglobul
42	234.2	53.6	891	21	AAZ78320 Anti-human Fas Ig
43	231.8	53.0	1497	24	AAZ97145 3B10xP4-3 bispecif
44	231.8	53.0	1509	24	AAZ97146 3B10xP4-14 bispecif
45	231.8	53.0	1509	24	AAZ97147 3B10xP5-2 bispecif

ALIGNMENTS

RESULT 1
AAZ34746
ID AAZ34746 standard; cDNA; 437 BP.
XX
AC AAZ34746;
XX
DT 15-FEB-2000 (first entry)
DE
DE Mouse anti-CD23 MAB C11 light chain variable region cDNA.
XX
KW CD23; FCERII; IGF receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes;
KW B-cell malignancy; therapy; ds.
XX
OS Mus musculus.

XX	Key	Location/Qualifiers
FT	CDS	3..413
FT		/*tag= a
XX		
PN	WO9958679-A1.	
XX		
PD	18-NOV-1999.	
XX		
PF	07-MAY-1999;	99WO-GB01434.

XX 09-MAY-1998; 98GB-0009839.
XX (GLAX) GLAXO GROUP LTD.
XX PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
XX DR WPI; 2000-053101/04.
XX P-PSDB; AAY32261.
XX Cell receptor specific antibodies useful for treating e.g. arthritis,
XX diabetes, multiple sclerosis and psoriasis -
XX Claim 16; Fig 2; 81pp; English.
XX This DNA sequence encodes the light chain variable region (VL) of
XX murine anti-CD23 (FCERI) monoclonal antibody C11. The invention
XX provides altered antibodies, such as chimeric or humanised
XX antibodies (see AAY34747 and AAY34748), which comprise sufficient of
XX the amino acid sequences of the C11 light and heavy chain
XX complementary determining regions (see AAY32254-59) to render them
XX capable of binding to the CD23 type II molecule expressed on
XX haematopoietic cells. The antibodies are used to block soluble
XX CD23 formation in human therapy, for the treatment of arthritis,
XX lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
XX diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
XX syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
XX colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
XX asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
XX eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
XX (particularly chronic bronchitis) or diabetes (particularly type 1
XX diabetes), and B-cell malignancies (claimed). They are also useful
XX for studying interactions between CD23 and various ligands and
XX determining the binding agents.
XX Sequence 437 BP; 108 A; 93 C; 114 G; 122 T; 0 other;

Query Match 100.0%; Score 437; DB 21; Length 437;
Best Local Similarity 100.0%; Pred. No. 3.6e-124;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGTCTCTGTTCAGTTTCGG 60
Db 1 AAGCTTTACAGTTACTCAGCACACAGGACCTCACCATGAGTCTCTGTTCAGTTTCGG 60
Qy 61 GGGTGCTTATGTTCTGGATCTCTGGATCAGTGGGGATATTGATTAACCCAGGATGAAC 120
Db 61 GGGTGCTTATGTTCTGGATCTCTGGATCAGTGGGGATATTGATTAACCCAGGATGAAC 120
Qy 121 TCTCAATCCCTGTCACCTTCTGGAGAATCAGTTTCCATCTCTGCAGTCTAGTAAGATC 180
Db 121 TCTCAATCCCTGTCACCTTCTGGAGAATCAGTTTCCATCTCTGCAGTCTAGTAAGATC 180
Qy 181 TCCTGTATAGGATGGAAGACATACCTTGAATGGTTTCTGCAGACACCAAGCAATCTC 240
Db 181 TCCTGTATAGGATGGAAGACATACCTTGAATGGTTTCTGCAGACACCAAGCAATCTC 240
Qy 241 CTCAGTCCCTGATGATTTGATGTCACCCGTCGATCAGAGTCTCAGACCGGTTAGTG 300
Db 241 CTCAGTCCCTGATGATTTGATGTCACCCGTCGATCAGAGTCTCAGACCGGTTAGTG 300
Qy 301 GCAGTGGGTGAGGACAGATTTTCCCTCGGAATCAGTACAGTGAAGCTGAGGATGTGG 360
Db 301 GCAGTGGGTGAGGACAGATTTTCCCTCGGAATCAGTACAGTGAAGCTGAGGATGTGG 360
Qy 361 GTGTGTATTACTGTCACAACTTGTAGAGTATCCATTACGTTTCGGTCGGGGACAAAGT 420
Db 361 GTGTGTATTACTGTCACAACTTGTAGAGTATCCATTACGTTTCGGTCGGGGACAAAGT 420
Qy 421 TGGAAATAAACAACGTACG 437
Db 421 TGGAAATAAACAACGTACG 437

RESULT 2
AAQ12056
ID AAQ12056 standard; DNA; 429 BP.
XX AC AAQ12056;
XX 15-AUG-1991 (first entry)
XX Sequence encoding light (kappa) chain variable region of murine
XX 2E12 immunoglobulin.
XX Chimeric antibodies; immunoconjugates; HIV; AIDS; ss.
XX Mus musculus.
XX Key Location/Qualifiers
XX CDS 34..429
XX /*tag= a
XX /product= mouse MAb 2E12 L(kappa)-chain
XX variable region
XX WO9107493-A.
XX 30-MAY-1991.
XX 13-NOV-1990; 90WO-US06615.
XX 13-NOV-1989; 89US-0433730.
XX (XOMA-) XOMA CORP.
XX (GREC) GREEN CROSS CORP.
XX Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
XX WPI: 1991-178044/24.
XX P-PSDB; AAR12354.
XX New chimeric mouse-human antibodies - used to detect, kill and
XX remove HIV-1 antigen from sample
XX Disclosure; fig 1; 107pp; English.
XX This sequence encodes the light (kappa)- chain variable (V) region
XX of a mouse monoclonal antibody (MAb), 2E12, specific for an HIV-1
XX viral antigen. It is used in the construction of a chimeric MAb
XX comprising heavy and light chains having murine V regions and human
XX C regions. The chimeric MABs are more effective than murine MAB
XX 2E12 since they have an increased compatibility in humans. The
XX heavy and light chain V-regions are joined by manipulating their
XX respective joining (J) regions, to generate restriction enzyme
XX recognition sites. The chimeric MABs can be used as immuno-
XX conjugates, in association with e.g. toxins for HIV treatment.
XX They can also be used in diagnosis of HIV.
XX See also AAQ12057-63.
XX Sequence 429 BP; 103 A; 92 C; 120 G; 114 T; 0 other;

Query Match 83.8%; Score 366.4; DB 12; Length 429;
Best Local Similarity 93.6%; Pred. No. 1.7e-102;
Matches 382; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Qy 24 CAGGACCTCACCATGAGTCTCTCTTTCAGTTTCTGGGGGCTTATGTTCTGGATCTCT 83
Db 22 CAAGTCTCAGAAATGAGTGTCTCTTCTCAGTTTCTGGGGGCTTATGTTCTGGATCTCT 81
Qy 84 GGAGTCAGTGGGGATATTCTGATAACCCAGGATGAACCTCCTCAATCCTGTCACTTCTGGA 143
Db 82 GGAGTCAGTGGGGATATTCTGATAACCCAGGATGAACCTCCTCAATCCTGTCACTTCTGGA 141
Qy 144 GAATCAGTTTCCATCTCTCGAGGTCCTAGTAGAGTCTCCTGTATAGGATGGGAAGACA 203
Db 142 GAATCAGTTTCTCTCTCTCGAGGTCCTAGTAGAGTCTCCTGTATAGGATGGGAAGACA 201

```
QY 204 TACTTGAATTGGTTTCTGCAGAGACCAGGACAATCTCCTCAGCTCCTGATGTTATTTGATG 263
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 202 TACTTGAATTGGTTTCTGCAGAGACCAGGACAATCTCCTCAGCTCCTGATCTATCTGATG 261
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 264 TCCACCCGTCATCAGAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGCACAGATTTTC 323
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 262 TCCACCCGTCATCAGAGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGCACAGATTTTC 321
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 324 ACCCTGGAATCACTAGAGTGAAGGCTGAGGATCTGGGCTGTGTTACTCTCAACAACCTT 383
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 322 ACCCTGGAATCACTAGAGTGAAGGCTGAGGATCTGGGCTGTGTTACTCTCAACAACCTT 381
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 384 GTAGAGTATCATTCAGTTTCGGCTCGGGGACAAAGTTGGAAATAAAA 431
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 382 GTAGAGTATCGTACACATTCGGAGGGGGACCAAGCTGGAATAAAA 429
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
AAQ12012
ID AAQ12012 standard; DNA; 429 BP.
XX AC AAQ12012;
XX OS
DT 19-AUG-1991 (first entry)
XX DE
XX KW HIV-1; chimera; ds.
XX OS
XX FH Key Location/Qualifiers
XX FT CDS 34..429
XX FT /*tag= a
XX FN WO9107494-A.
XX PD
XX PE 30-MAY-1991.
XX PR 13-NOV-1990; 90WO-US06627.
XX PR 13-NOV-1989; 89US-0433703.
XX PA (XOMA-) XOMA CORP.
XX PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
XX DR WPI; 1991-178106/24.
XX DR P-PSDB; AARI2232.
XX PT New chimeric mouse human antibodies - used in treatment, diagnosis
XX PT and prophylaxis of HIV infections.
XX PS Disclosure; Fig 1; 108pp; English.
XX CC The mouse VL gene product may be used to produce chimeric mouse-
XX CC human Abs against HIV-1 comprising human Ig constant regions and
XX CC murine variable regions. These novel sequence are useful in
XX CC treatment, diagnosis and prophylaxis of HIV infections, and may be
XX CC produced by a bacterial, yeast or mammalian expression system.
XX SQ Sequence 429 BP; 103 A; 92 C; 120 G; 114 T; 0 other;

Query Match 83.8%; Score 366.4; DB 12; Length 429;
Best Local Similarity 93.6%; Pred. No. 1.7e-102;
Matches 382; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 24 CAGGACCTCACCATCAGGTTCTCTGTTTCAGTTTCTGGGGTGCCTATGTTCTGGATCTCT 83
    || ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 22 CAAGTTCTCAGAATCAGGTGCTCTCTTCAGTTCTCCTGGGGTGCCTATGTTCTGGATCTCT 81
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 84 GAGTCACTGGGGATATTGTGATATACCCAGGATGACTCTCCACTCTGCTCACTTCTGGA 143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
Db 82 GGAGTCAGTGGGAGATTGTGATAACCCAGGATGAATCTCCAAATCCTGTCTCTTCTGGA 141
QY 144 GAATCAGTTTCCATCTCCTGCAGAGTCTAGTAAGAGTCTCCTGTATAAGSAGGGAACA 203
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 142 GAATCAGTTTCCATCTCCTGCAGAGTCTAGTAAGAGTCTCCTGTATAAGSAGGGAACA 201
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 204 TACTTGAATTGGTTTCTGCAGAGACCAGGACAATCTCCTCAGCTCCTGATGTTATTTGATG 263
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 202 TACTTGAATTGGTTTCTGCAGAGACCAGGACAATCTCCTCAGCTCCTGATCTATCTGATG 261
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 264 TCCACCCGTCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGCACAGATTTTC 323
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 262 TCCACCCGTCATCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGCACAGATTTTC 321
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 324 ACCCTGGAATCAGTAGAGTGAAGGCTGAGGATCTGGGCTGTGTTACTCTCAACAACCTT 383
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 322 ACCCTGGAATCAGTAGAGTGAAGGCTGAGGATCTGGGCTGTGTTACTCTCAACAACCTT 381
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 384 GTAGAGTATCATTCAGTTTCGGCTCGGGGACAAAGTTGGAAATAAAA 431
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 382 GTAGAGTATCGTACACATTCGGAGGGGGACCAAGCTGGAATAAAA 429
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
AAV09791
ID AAV09791 standard; cDNA; 340 BP.
XX AC AAV09791;
XX DT 16-JUN-1998 (first entry)
XX DE
XX KW DNA encoding the light chain of the catalytic antibody 3B9.
XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
XX KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX KW overdose; addiction; ss.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT CDS 1..340
XX FT /*tag= a
XX FT /note= "no stop codon given"
XX PN WO9749800-A1.
XX PD 31-DEC-1997.
XX PF 25-JUN-1997; 97WO-US10965.
XX PR 25-JUN-1996; 96US-0672345.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Landry DW;
XX WPI; 1998-077166/07.
XX DR P-PSDB; AAW39801.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required
XX PT in far smaller doses than antibodies that antagonise cocaine by
XX PT simply binding
XX PS Disclosure; Fig 17; 147pp; English.
XX CC The present sequence encodes the light chain of a catalytic antibody
XX CC which is capable of degrading cocaine. A series of cocaine transition
XX CC state analogues (TSAs) were prepared and used to immunise mice for
XX CC production of hybridomas. Catalytic antibodies were identified by their
XX CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
XX CC antibodies reduce the concentration of cocaine in a subject, and are used
```

CC particularly for the treatment of an overdose. They are also used for
CC treating addiction (by reducing the in vivo concentration that can be
CC achieved).

Query Match	72.6%	Score 317.2;	DB 19;	Length 340;
Best Local Similarity	96.2%	Pred. NO. 2e-87;		
Matches 325;	Conservative	0;	Mismatches 13;	Indels 0;
Gaps	0;			

Qy 96 GATATTGTGATAACCCAGGATGAACCTCTCCAATCCTGTCACTTCTGGAGAATCACTTCC 155
|||||
Db 1 GATATTGTGATACCCAGGATGAACCTCTCCAATCCTGTCACTTCTGGAGAATCACTTCC 60

PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX
PS Disclosure; Flg 21: 147pp; English.

Query Match	72.6%	Score 317.2;	DB 19;	Length 368;
Best Local Similarity	96.2%	Pred. No. 2.11e-87;		
Matches 325;	Conservative	0;	Mismatches 13;	Indels 0;
			Gaps	0;

Qy 96 GATATTGTATAACCAAGGATGAACCTCCAATCCTGTCACTTCTGGAGAATCAGTTTC 155
 ||||| ||||| | | | | | | | | | | | | | | | |
Dd 1 GATATGGTGATGACCGAAGACAACACTCCAATCCTGTCACTTCTGGAGAAATCAGTTTC 60

PF 25-JUN-1997; 97WO-US10965.
XX
PR 25-JUN-1996; 96US-0672345.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Landry DW;
XX
DR WPI: 1998-077166/07.
DR P-PSDB; AAW39803.
XX
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX
XX Disclosure; Fig 23; 147pp; English.
XX
XX The present sequence encodes the light chain of a catalytic antibody
CC which is capable of degrading cocaine. A series of cocaine transition
CC state analogues (TSAs) were prepared and used to immunise mice for
CC production of hybridomas. Catalytic antibodies were identified by their
CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
CC antibodies reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used for
CC treating addiction (by reducing the in vivo concentration that can be
CC achieved).
XX
SQ Sequence 420 BP; 98 A; 95 C; 115 G; 108 T; 4 other;

Query Match 72.3%; Score 316; DB 19; Length 420;
Best Local Similarity 95.6%; Pred. No. 5.1e-87;
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 94 GGGATATTGTGATACCCAGGATGAACCTCCCAATCCTGTCACTCTCGGAGAACATCAGTTT 153
DB 51 GCGATAGTGTGATGACGAGGATGAACCTCCCAATCCTGTCACTCTCGGAGAACATCAGTTT 110

QY 154 CCATCTCCTCGCAGGCTAGTAAAGAGTCTCCTGTATAGGATGGGAAGACATCTTGAATT 213
DB 111 CCATCTCCTCGCAGGCTAGTAAAGAGTCTCCTGTATAGGATGGGAAGACATCTTGAATT 170

QY 214 GGTTCCTCGCAGACAGGACATCTCCTCAGCTCCTCATGTATTGTATGTCACCCGTTG 273
DB 171 GGTTCCTCGCAGACAGGACATCTCCTCAGCTCCTCATGTATTGTATGTCACCCGTTG 230

QY 274 CATCAGGAGTCTCAGACCGTTTACTGGCAGTGGGTGAGGACAGATTTACCTCGGAAA 333
DB 231 CATCAGGAGTCTCAGACCGTTTACTGGCAGTGGGTGAGGACAGATTTACCTCGGAAA 290

QY 334 TCAGTAGAGTGAAGGCTGAGGATGGGTGTGTATTACTGTCAACAACCTGTAGAGTATC 393
DB 291 TCAGTAGAGTGAAGGCTGAGGATGGGTGTGTATTACTGTCAACAACCTTTGTAGACTATC 350

QY 394 CATTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAAACG 433
DB 351 CATTCACGTTCCGCTCGGGGACAAAGTTGGAGATAAAACG 390

RESULT 7
AAV09793
ID AAV09793 standard; cDNA; 368 BP.
XX
AC AAV09793;
XX
XX 18-JUN-1998 (first entry)
DT
XX DNA encoding the light chain of the catalytic antibody 6A12.
DE
XX Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction; ss.

XX Mus sp.
OS
XX
FH Key Location/Qualifiers
FT CDS I..339
FT /*tag= a
FT /note= "no stop codon given"
XX
PN W09749800-A1.
XX
PD 31-DEC-1997.
XX
XX 25-JUN-1997; 97WO-US10965.
XX
XX 25-JUN-1996; 96US-0672345.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Landry DW;
PI
XX WPI: 1998-077166/07.
DR P-PSDB; AAW39886.
XX
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX
XX Disclosure; Fig 19; 147pp; English.
XX
XX The present sequence encodes the light chain of a catalytic antibody
CC which is capable of degrading cocaine. A series of cocaine transition
CC state analogues (TSAs) were prepared and used to immunise mice for
CC production of hybridomas. Catalytic antibodies were identified by their
CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
CC antibodies reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used for
CC treating addiction (by reducing the in vivo concentration that can be
CC achieved).
XX
SQ Sequence 368 BP; 95 A; 80 C; 93 G; 100 T; 0 other;

Query Match 70.8%; Score 309.2; DB 19; Length 368;
Best Local Similarity 94.7%; Pred. No. 6e-85;
Matches 320; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 96 GATATTGTGATACCCAGGATGAACCTCCCAATCCTGTCACTCTCGGAGAACATCAGTTTCC 155
DB 1 GATATTGTGATGAGCGGAGATGAACCTCCCAATCCTGTCACTCTCGGAGAACATCAGTTTCC 60

QY 156 ATCTCTCGCAGGCTAGTAAAGAGTCTCCTGTATAGGATGGGAAGACATCTTGAATTGG 215
DB 61 ATCTCTCGCAGGCTAGTAAAGAGTCTCCTGTATAGGATGGGAAGACATCTTGAATTGG 120

QY 216 TTCTCGCAGACAGGACATCTCCTCAGCTCCTCATGTATTGTATGTCACCCGTTGCA 275
DB 121 TTCTCGCAGACAGGACATCTCCTCAGCTCCTCATGTATTGTATGTCACCCGTTGCA 180

QY 276 TCAGGAGTCTCAGACCGTTTACTGGCAGTGGGTGAGGACAGATTTACCTCGGAAATC 335
DB 181 TCAGGAGTCTCAGACCGTTTACTGGCAGTGGGTGAGGACAGATTTACCTCGGAAATC 240

QY 336 AGTAGAGTGAAGGCTGAGGATGGGTGTGTATTACTGTCAACAACCTTTGTAGAGTATCCA 395
DB 241 AGTAGAGTGAAGGCTGAGGATGGGTGTGTATTACTTTCAACACTTTTGAAGACTATCCA 300

QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAAATAAAACG 433
DB 301 TTCACGTTCCGCTCGGGGACAAAGTTGGAGATAAAACG 338

RESULT 8
AAQ33097


```
FT CDS 40..441
XX /*tag= a
PN WO9002569-A.
XX
XX 22-MAR-1990.
XX
XX 06-SEP-1989; 89WO-US03852.
XX
XX 06-SEP-1988; 88US-0240624.
XX 08-SEP-1988; 88US-0241744.
XX 13-SEP-1988; 88US-0243739.
XX 04-OCT-1988; 88US-0253002.
XX 19-JUN-1989; 89US-0367641.
XX 21-JUL-1989; 89US-0382768.
XX
XX (ITGE-) INT GENETIC ENG INC.
XX
XX Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
XX WPI; 1990-115825/15.
XX P-PSDB; AAR09420.
XX
XX Chimeric mouse-human antibodies - prepd. using genes coding for
XX constant human region murine variable region, esp. to 3 tumour
XX antigen
XX
XX Claim 13; Page 123 + Fig 7; 173pp; English.
XX
XX Shown is the nucleotide sequence from the end of the oligo-dC tail
XX to the Jk1-Ck junction. The sequence is used in the prodn. of a
XX chimeric antibody mol. comprising two light chains and two heavy chains,
XX each having a constant region (human) and a variable region (murine)
XX having specificity to an antigen bound by murine monoclonal antibody
XX (Mab) B38.1. The chimeric antibodies can be used for any purpose for
XX which the original murine MAbs can be used, with the advantage that
XX they are more compatible with the human body. They are esp. used for
XX the diagnosis and treatment of cancer.
XX
XX SQ Sequence 441 BP; 101 A; 106 C; 114 G; 120 T; 0 other;
XX
XX Query Match 63.4%; Score 277.2; DB 11; Length 441;
XX Best Local Similarity 79.8%; Pred. No. 4.3e-75;
XX Matches 327; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
XX
QY 24 CAGGACCTCACCATGAGGTTCTCTGTTCAGTTCTGGGGTGCTTATGTTGATCTCT 83
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 28 CAAGTTCGAGAATGAGGTTCTCTGTCTCAGCTTCTGGGGTGCTTGTGCTGATCCCT 87
XX
QY 84 GGAGTCAGTGGGATATTTGATATACCCAGGATGAACCTCTCCAAATCCTGCTACTTCTGA 143
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 88 GGATCCACTGCAGATATTTGATGACGCGAGGCTGCATTTCTCCAAATCAGTCACTTTGA 147
XX
QY 144 GAATCAGTTTCCATCTCTCCTCAGGTTCTAGTAAGAGTCTCTGTATAGGATGGGAAGACA 203
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 148 ACATCAGGTTCCATCTCTCCTCAGGTTCTAGTAAGAGTCTCTCATAGTAAATGCACTACT 207
XX
QY 204 TACTTGAATTTGGTTTCGACAGACCAGGACAATCTCTCAGTCTCTGTATGTTATTTGATG 263
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 208 TATTTGATTTGGTATCTGCAGAGACGAGGCCAGTCTCTCAGTCTCTGATTTATCAGATG 267
XX
QY 264 TCCACCCGTCATCAGAGTCTCAGACCCGTTTATGTTGGCAGTGGGTCAGGCACAGATTTC 323
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 268 TCCAACTTCTGCCAGAGTCCAGACAGGTTTCAGTAGCAGTGGGTCAGGAACGTGATTTTC 327
XX
QY 324 ACCCTGAAATCAGTAGGAGGCTGAGGATGTGGGTGTGTTATCTACATCAACAACCTT 383
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 328 ACTAGATATCAGCAGAGTGGAGGCTGAGATGTGGGTGTTTATCTACTGCTCAAAAT 387
XX
QY 384 GTAGAGTATCCATTCAGTTTCGGCTCGGGGACAAAGTTGGAAATATAAACG 433
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 388 CTAGAACTTCTCGGACGTTTCGGTGGAGGACCAAGCTGGAATCAAAACG 437
```

```
RESULT 12
AAT43434
ID AAT43434 standard; cDNA; 441 BP.
XX
XX AAT43434;
AC
XX
XX 12-FEB-1997 (first entry)
XX
XX Mab B38-1 light chain variable region cDNA.
XX
XX Chimeric antibody; monoclonal antibody; B38.1;
XX antibody engineering; tumour; antigen; breast carcinoma;
XX lung carcinoma; colon carcinoma; ovary carcinoma; cancer;
XX diagnosis; therapy; light chain; ss.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX FH 40..441
XX FT /*tag= a
XX FT /product= B38.1 light chain V region
XX
XX US5576184-A.
XX
XX PD 19-NOV-1996.
XX
XX 06-SEP-1988; 88US-0240624.
XX
XX 06-MAY-1991; 91US-0659401.
XX 06-SEP-1988; 88US-0240624.
XX 08-SEP-1988; 88US-0241744.
XX 13-SEP-1988; 88US-0243739.
XX 04-OCT-1988; 88US-0253002.
XX 19-JUN-1989; 89US-0367641.
XX 21-JUL-1989; 89US-0382768.
XX 27-DEC-1994; 94US-0364001.
XX
XX (XOMA ) XOMA CORP.
XX
XX Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
XX WPI; 1997-011249/01.
XX P-PSDB; AAW06209.
XX
XX Chimeric mouse-human antibodies - recognise a human tumour antigen,
XX used for the treatment and diagnosis of human cancers
XX
XX Example 3; Fig 7; 102pp; English.
XX
XX A cDNA clone (AAT43434) codes for the light chain variable region
XX (AAW06209) of mouse monoclonal antibody (Mab) B38-1, and extends from
XX the end of the oligo-dC tail to the J kappa-C kappa junction. It
XX was obt'd. from a B38-1 hybridoma cDNA library by screening with a
XX mouse C kappa region probe. Mab B38.1 (IgG1) binds to an antigen
XX that is expressed on the surface of human lung, breast, colon and
XX ovary carcinomas, but not on normal adult tissues. Light chain and
XX heavy chain variable region (see also AAT43435-43) sequences can be
XX used with human constant region sequences to express mouse-human
XX chimeric antibodies in transformed host cells. The antibodies have
XX specificity to human tumour antigens and can be used for the
XX treatment and diagnosis of human cancer.
XX
XX SQ Sequence 441 BP; 101 A; 106 C; 114 G; 120 T; 0 other;
XX
XX Query Match 63.4%; Score 277.2; DB 18; Length 441;
XX Best Local Similarity 79.8%; Pred. No. 4.3e-75;
XX Matches 327; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
XX
QY 24 CAGGACCTCACCATGAGGTTCTCTGTTCAGTTCTGGGGTGCTTATGTTGATCTCT 83
DB 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
DB 28 CAAGTTCGAGAATGAGGTTCTCTGCTCAGCTTCTGGGGTGCTTGTGCTGATCCCT 87
```

```

QY 84 GGAGTCAGTGGGGATATTGTGATACCCAGCATGAATCTCCAAATCCTGCTCACTTCGGA 143
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 88 GGATCCACTGAGATATTGTGATGCGAGCGCTGCATCTCCAAATCCAGTCACTTCGGA 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
QY 144 GAATCAGTTTCCATCTCTCGAGGTCCTAGTAAAGAGTCTCTCTGTATAGAGTGGGAAGACA 203
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 148 ACATCAGGTTCCATCTCTCGAGGTCCTAGTAAAGAGTCTCTCTACATAGTAAATGGCATCACT 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
QY 204 TACTTGAATTTGTTCTCCAGAGCAGGACAATCTCTCAGCTCCCTGATGATTTGATG 263
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 208 TATTGTATTGTTATCTCGAAGCCAGGCGAGTCTCTCAGCTCCCTGATTTATCAGATG 267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
QY 264 TCCACCCGTCATCAGGAGTCTCAGACCGGTTTATGTGSCAGTGGGTGAGGACAGATTTTC 323
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 268 TCCAACTTGGCTCAGGAGTCCCAGACAGGTTTCAGTAGCAGTGGGTGAGGAACATGATTC 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
QY 324 ACCCTGGAAATCAGTAGAGTGAAGCTCAGGATGTGGGTGTGATTAAGTCTGACACACTT 383
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 328 ACACGTGAGAATCAGCAGAGTGGAGCTGAGGATGTGGGTGTGATTAAGTCTGCTCAAAAT 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
QY 384 GTAGAGTATCCATTCACGTTCCGGCTCGGGGACAAAGTTGGAAATAAAACG 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 388 CTAGAACTTCTCGGACGCTTCGGTGGAGGCACCAAGCTGGAATCAACG 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||

RESULT 13
AAV71152
ID AAV71152 standard; DNA; 441 BP.
XX
AC AAV71152;
XX
DT 16-APR-1999 (first entry)
XX
DE Coding strand for mouse B38.1 light chain variable region.
XX
KW Light chain variable region; murine antibody B38.1; antibody ING-1;
KW chimeric immunoglobulin; human tumour antigen; chimeric antibody;
KW treatment; human cancer; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 40..441
FT /*tag= a
FT /note= "partial CDS, no termination codon given"
XX
PN US5843685-A.
XX
PD 01-DEC-1998.
XX
PF 06-JUN-1995; 95US-0466034.
XX
PR 06-SEP-1989; 89WO-US03852.
XX
PR 06-SEP-1988; 88US-0240624.
XX
PR 08-SEP-1988; 88US-0241744.
XX
PR 13-SEP-1988; 88US-0243739.
XX
PR 04-OCT-1988; 88US-0253002.
XX
PR 19-JUN-1989; 89US-0367641.
XX
PR 21-JUL-1989; 89US-0382768.
XX
PR 27-DEC-1994; 94US-0364001.
XX
PR 06-JUN-1995; 95US-0466034.
XX
PA (XOMA ) XOMA CORP.
XX
PI Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
XX
XX WPI; 1999-044574/04.
XX
DR P-PSDB; AAW85056.
XX
PT Chimeric antibody specific for human tumour antigen - useful as
PT immunoassay, imaging or antitumour agent
XX
PS Example 3; Fig 7; 92pp; English.

```

```

XX The present sequence encodes the light chain variable region of
CC murine antibody B38.1. The sequence was used to create chimeric
CC mouse-human immunoglobulins which recognise the human tumour
CC antigen bound by antibody ING-1 (produced by hybridoma cell line
CC ATCC HB 9812). The chimeric antibodies also have an antigen-binding
CC site that competitively inhibits the binding of antibody ING-1, and
CC mediate complement-dependent cytotoxicity of target cells or
CC antibody-dependent cellular cytotoxicity to target cells. The
CC chimeric antibodies can be used for therapeutic purposes in the
CC treatment of human cancer.
XX
SQ Sequence 441 BP; 101 A; 106 C; 114 G; 120 T; 0 other;
    Query Match 63.4%; Score 277.2; DB 20; Length 441;
    Best Local Similarity 79.8%; Pred. No. 4.3e-75;
    Matches 327; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 24 CAGGACCTCACCATGAGGTTCTCTGTTCAGTTTCTGGGGTGCTTATGTTCTGGATCTCT 83
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 28 CAAGTTGCGAGAATGAGTTCTCTGCTCAGCTTCTGGGGTGCTTGTGCTCGATCCCT 87
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
QY 84 GGAGTCAGTGGGGATATTGTGATAACCCAGGATGAATCTCCAAATCCTGCTCACTTCGGA 143
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 88 GGATCCACTGCAATATTGTGATGAGCGAGGCTGCATTTCCCAATCCAGTCACTTCGGA 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
QY 144 GAATCAGTTTCCATCTCTCAGGTCCTAGTAAAGAGTCTCTGTATAGAGTGGGAAGACA 203
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 148 ACATCAGGTTCCATCTCTCAGGTCCTAGTAAAGAGTCTCTACATAGTAAATGGCATCACT 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
QY 204 TACTTGAATTTGTTCTTCGAGAGCAGGACAATCTCTCAGCTCCCTGATGATTTGATG 263
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 208 TATTGTATTGTTATCTCGAAGCCAGGCTGAGGATGTGGGTGTGATTAAGTCTGCTCAAAAT 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
QY 264 TCCACCCGTCATCAGGAGTCTCAGACCGGTTTATGTGSCAGTGGGTGAGGACAGATTTTC 323
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 268 TCCAACTTGGCTCAGGAGTCCCAGACAGGTTTCAGTAGCAGTGGGTGAGGAACATGATTC 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
QY 324 ACCTGGAAATCAGTAGAGTGAAGCTCAGGATGTGGGTGTGATTAAGTCTGCTCAAAAT 383
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 328 ACACGTGAGAATCAGCAGAGTGGAGCTGAGGATGTGGGTGTGATTAAGTCTGCTCAAAAT 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
QY 384 GTAGAGTATCCATTCACGTTTCGGCTCGGGGACAAAGTTGGAAATAAAACG 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||
DB 388 CTAGAACTTCTCGGACGCTTCGGTGGAGGCACCAAGCTGGAATCAACG 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||

RESULT 14
AAQ38878
ID AAQ38878 standard; cDNA; 399 BP.
XX
AC AAQ38878;
XX
DT 16-JUL-1993 (first entry)
XX
DE CTMO1 VL cDNA.
XX
KW Heavy; light; chain; variable; domain; CTMO1; PCR; primer; carcinoma;
KW immunoglobulin; murine; monoclonal; antibody; MAb; IgG-kappa; ovary;
KW humanised; diagnosis; therapy; breast; uterus; lung; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT sig_peptide 1..60
FT /*tag= a
FT mat_peptide 61..399
FT /*tag= b
XX
PN EP534742-A.
XX
PD 31-MAR-1993.
XX

```


GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 07:27:07 ; Search time 42.2347 Seconds
(without alignments)
11258.801 Million cell updates/sec

Title: US-09-674-716B-2

Perfect score: 437

Sequence: 1 aagctttaccagttactcagc.....agttggaaataaaacgtacg 437

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 709820 seqs, 544064369 residues

Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA.*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	247	56.5	968	9	US-09-924-340-7
2	247	56.5	968	9	US-09-992-600A-7
3	245.2	56.1	738	9	US-10-158-646-61
4	241.2	55.2	954	9	US-09-479-614-19
5	241.2	55.2	954	9	US-09-479-614-21
6	238.4	54.6	726	9	US-09-479-614-23
7	238.4	54.6	726	9	US-09-479-614-24
8	223.6	51.2	399	10	US-09-905-243-55
9	222.8	51.0	2272	9	US-10-158-646-63
10	220.4	50.4	413	10	US-09-748-960-7
11	218.6	50.0	420	9	US-09-341-894-3
12	217.4	49.7	492	9	US-10-060-036-3813
13	214	49.0	420	10	US-09-881-823-9
14	211.6	48.4	720	9	US-10-124-905-5
15	211.6	48.4	720	9	US-09-948-429B-5
16	211.6	48.4	720	9	US-10-073-138-3
17	210.8	48.2	723	9	US-09-988-115A-60
18	210.4	48.1	396	10	US-09-748-960-1
19	208.6	47.7	729	12	US-10-006-773-10

20	205	46.9	384	10	US-09-753-436-44	Sequence 44, Appl
21	204.2	46.7	447	10	US-09-990-205-1	Sequence 1, Appl
22	204.2	46.7	504	12	US-10-006-773-14	Sequence 14, Appl
23	203.6	46.6	426	10	US-09-840-459-95	Sequence 95, Appl
24	203.6	46.6	426	10	US-09-840-459-101	Sequence 101, Appl
25	202.8	46.4	375	10	US-09-753-436-65	Sequence 65, Appl
26	202	46.2	339	10	US-09-822-698A-2	Sequence 2, Appl
27	202	46.2	663	10	US-09-822-698A-25	Sequence 25, Appl
28	202	46.2	1143	10	US-09-822-698A-6	Sequence 6, Appl
29	200.8	45.9	666	9	US-09-479-614-25	Sequence 25, Appl
30	200.8	45.9	666	9	US-09-479-614-27	Sequence 27, Appl
31	198	45.3	563	10	US-09-864-761-15798	Sequence 15798, A
32	196.6	45.0	573	10	US-09-864-761-15819	Sequence 15819, A
33	195.6	44.8	344	10	US-09-840-459-98	Sequence 98, Appl
34	195.6	44.8	344	10	US-09-840-459-105	Sequence 105, Appl
35	194	44.4	749	9	US-09-968-851-46	Sequence 46, Appl
36	194	44.4	1611	9	US-09-968-851-37	Sequence 37, Appl
37	193.2	44.2	568	10	US-09-864-761-15969	Sequence 15969, A
38	193	44.2	476	10	US-09-864-761-32306	Sequence 32306, A
39	192.8	44.1	335	10	US-09-864-761-32327	Sequence 32327, A
40	192	43.9	588	10	US-09-864-761-15896	Sequence 15896, A
41	191.2	43.8	336	9	US-09-848-798-99	Sequence 99, Appl
42	187.6	42.9	879	10	US-09-978-752-22	Sequence 22, Appl
43	187.4	42.9	1135	9	US-09-203-958-2	Sequence 2, Appl
44	185.8	42.5	572	10	US-09-864-761-8081	Sequence 8081, Ap
45	185.2	42.4	723	10	US-09-978-752-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-924-340-7
; Sequence 7, Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephanie
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US2.REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 7
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..31
; NAME/KEY: CDS
; LOCATION: 32..748
; NAME/KEY: 3'UTR
; LOCATION: 749..968
; NAME/KEY: polyA.signal
; LOCATION: 928..933
; NAME/KEY: polyA.site
; LOCATION: 953..968
US-09-924-340-7

Query Match 56.5%; Score 247; DB 9; Length 968;
Best Local Similarity 75.4%; Pred. No. 1.6e-73;
Matches 307; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

```
QY 30 CTCACATGAGGTTCTCTGTTTCAGTCTTTCTGGGGGTGCTTATGTTCTGATCTCTGGAGTC 89
Db 26 CTCACAATGAGGCTCCCTGCTCAGCTCCTGGGCTGCTAATGCTCTGGGCTCTGGATCC 85
QY 90 AGTGGGATATTGATGAACCCAGGATGAACCTCCCAATCCTGCTCACTTCTGGAGATCA 149
Db 86 AGTGGGATATTGATGAACCTCACTGCTCCCACTCTTCTGCGCCGTGACCCCTGGAGAGCG 145
QY 150 GTTTCATCTCTCGAGGCTCTAGTAAGAGTCTCTCTGTATAGGATGGGAAGACATACTTG 209
Db 146 GCCTCCATCTCTCGAGGCTCTAGTCAGAGCTCTCTGTATGTTCAAGGGTCCAATATTG 205
QY 210 AATTGGTTTCTCGAGAGCAGGACAAATCTCTCAGCTCCTGATGATTTGATGTCCACC 269
Db 206 GATTGGTACCACCAAGAGCCAGGCGAGTCTCCACAACCTCTGATATACTTGGGTTCTAAT 265
QY 330 GAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTTACTGTCTCAACAACCTGTAGAG 389
Db 326 AAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTTACTGTCAATGCAAGCTCTACAA 385
QY 390 TATCCATTACGTTCCGCTCGGGGACAAAGTTGGAATAAAACGTAC 436
Db 386 ACTCCATTACCTTCGGCCCTGGGACCAAGAGTGGATATCAAGCGAAC 432
```

RESULT 2

```
US-09-992-600A-7
; Sequence 7, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91 US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992,600A
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Jpatent
; SEQ ID NO 7
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..31
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..748
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 749..968
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 928..933
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 953..968
```

US-09-992-600A-7

```
Query Match 56.5%; Score 247; DB 9; Length 968;
Best Local Similarity 75.4%; Pred. No. 1.6e-73;
Matches 307; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
QY 30 CTCACATGAGGTTCTCTGTTTCAGTCTTTCTGGGGGTGCTTATGTTCTGATCTCTGGAGTC 89
Db 26 CTCACAATGAGGCTCCCTGCTCAGCTCCTGGGCTGCTAATGCTCTGGGCTCTGGATCC 85
QY 90 AGTGGGATATTGATGAACCCAGGATGAACCTCCCAATCCTGCTCACTTCTGGAGATCA 149
Db 86 AGTGGGATATTGATGAACCTCACTGCTCCCACTCTTCTGCGCCGTGACCCCTGGAGAGCG 145
QY 150 GTTTCATCTCTCGAGGCTCTAGTAAGAGTCTCTCTGTATAGGATGGGAAGACATACTTG 209
Db 146 GCCTCCATCTCTCGAGGCTCTAGTCAGAGCTCTCTGTATGTTCAAGGGTCCAATATTG 205
QY 210 AATTGGTTTCTCGAGAGCAGGACAAATCTCTCAGCTCCTGATGATTTGATGTCCACC 269
Db 206 GATTGGTACCACCAAGAGCCAGGCGAGTCTCCACAACCTCTGATATACTTGGGTTCTAAT 265
QY 270 CGTGCATCAGGAGTCTCAGACCGGTTTACTGGCAGTGGGTGAGGCACAGATTTCAACCCTG 329
Db 266 CGGGCTCCGGGCTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTCAACACTG 325
QY 330 GAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTTACTGTCAACAACCTGTAGAG 389
Db 326 AAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTTACTGTCAATGCAAGCTCTACAA 385
QY 390 TATCCATTACGTTCCGCTCGGGGACAAAGTTGGAATAAAACGTAC 436
Db 386 ACTCCATTACCTTCGGCCCTGGGACCAAGAGTGGATATCAAGCGAAC 432
```

RESULT 3

```
US-10-158-646-61
; Sequence 61, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K.W.
; APPLICANT: Sornasse, Thierry
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0030-1 US
; CURRENT APPLICATION NUMBER: US/10/158,646
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/295,239
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PERL Program
; SEQ ID NO 61
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030073105A1 1329931.2
US-10-158-646-61
```

```
Query Match 56.1%; Score 245.2; DB 9; Length 738;
Best Local Similarity 76.6%; Pred. No. 5.7e-73;
Matches 314; Conservative 0; Mismatches 93; Indels 3; Gaps 1;
QY 30 CTCACATGAGGTTCTCTGTTTCAGTCTTTCTGGGGGTGCTTATGTTCTGATCTCTGGAGTC 89
Db 15 CTCACATGAGGCTCCCTGCTCAGCTCCTGGGCTGCTAATGCTCTGGGTCCCTGGGTCC 74
QY 90 AGTGGGATATTGATGAACCCAGGATGAACCTCCCAATCCTGCTCACTTCTGGAGATCA 149
Db 75 AGTGGGATATTGATGAACCCAGGATCCACGCTCCCTGCGCCGTGAGAGAGCG 134
QY 150 GTTTCATCTCTCGAGGCTCTAGTAAGAGTCTCTCTGTATATA--AGGATGGGAAGACATAC 206
```

Db 135 GCCTCCATCTCTCGAGGCTAGTCAGAGCCCTTCGATAGTATGATGATGGAACACCTAT 194
QY 207 TTGAATGGTTTCGAGAGACAGGACAATCTCCTCAGCTCTGATGATATTTGATGTC 266
Db 195 TTGGACTGGTACCTGCGAGAGCCAGGACGCTCCACAGCTCTGATCTATAGCTGTGCC 254
QY 267 ACCCGTGCATCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCACC 326
Db 255 CATCGGCGCTCTGGAGTCCACAGACAGGTTTCAGTGGCAGTGGTTCAGGCACTAATTTTCA 314
QY 327 CTGGAATCACTAGATGAAGCTGAGATGCTGGGTGTGTTACTGTCAACAACTTGTGA 386
Db 315 CTGAAATCAGCAGGGTGGAGGCTGACGATGTTGGAGTTTATTACTGCGATGCAACGTATA 374
QY 387 GAGTATCCATTCACGCTTCGGGCTCGGGGACAAAGTTGGAATAAAAGGTAC 436
Db 375 GAGTTCCGCTCACTTTCGGCGGAGGACCAAGGTAGATCAACAGAAC 424

RESULT 4

US-09-479-614-19
; Sequence 19, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479, 614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Felis catus
; NAME/KEY: CDS
; LOCATION: (7)..(732)
; FEATURE:
US-09-479-614-19

Query Match 55.2%; Score 241.2; DB 9; Length 954;

Best Local Similarity 74.6%; Pred. No. 1.4e-71;

Matches 303; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 30 CTCACCATGAGTCTCTGTTTCAGTCTTCTGGGGGTGCTTATGTTCTGGATCTCTGGAGTC 89
Db 1 CTCAAATGAGGTTCCCTGCTCAGCTCCTGGACTCATCATGCTCTGGATCCAGGATCC 60
QY 90 AGTGGGATATTTGATGAATCCAGGATGACTCTCCAAATCCTGTCACTTCTGGAGATCA 149
Db 61 AGTGGGATATTTGATGACGACAGCCCTCTGTCCCTGTCCGTCACCCCTGGAGACCA 120
QY 150 GTTTCATCTCTCGAGTCTAGTAAGAGTCTCCTGTATAGGATGGGACAGATCACTTG 209
Db 121 GCCTCAATCTCTCGAGGCCAGTCAGAGCCCTCTGTACAGTATGGAATATCTTATCTG 180
QY 210 AATGGTTTCTCGAGACAGGACAATCTCCTCAGCTCCTGATGATATTTGATGTCAC 269
Db 181 AATGGTACCTCGAGAGCCAGGACGCTCTCCAGGGGCTGTATCTTCTGTTTCCAA 240
QY 270 CCGTGCATCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCC 329
Db 241 CGGACTCTGGGTCCTCGAGAGGTTTCACTGGCAGTGGGTGAGGACAGATTTTCC 300
QY 330 GAAATCAGTAGAGTGAAGGCTGAGGATGCTGGGTGTGTTTACTGTCAACAACTTTAG 389
Db 301 AGAATCAGAGGCTGGAGGCTGACGACCTCGGTGTTTATTACTGCGGTCAAGGTTTAC 360
QY 390 TATCCATTCAGTCTCGGCTCGGGGACAAAGTTGGAATAAAACGTA 435

Db 361 CATCCTCTCACTTTCGCGCCAGGTACCAAGCTGGAGATCAACCGGA 406

RESULT 5

US-09-479-614-21/c
; Sequence 21, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479, 614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Felis catus
US-09-479-614-21

Query Match 55.2%; Score 241.2; DB 9; Length 954;

Best Local Similarity 74.6%; Pred. No. 1.4e-71;

Matches 303; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 30 CTCACCATGAGTCTCTGTTTCAGTCTTCTGGGGGTGCTTATGTTCTGGATCTCTGGAGTC 89
Db 954 CTCAAATGAGGTTCCCTGCTCAGCTCCTGGACTCATCATGCTCTGGATCCAGGATCC 895
QY 90 AGTGGGATATTTGATGAATCCAGGATGACTCTCCAAATCCTGTCACTTCTGGAGATCA 149
Db 894 AGTGGGATATTTGATGACGACAGCCCTCTGTCCCTGTCCGTCACCCCTGGAGACCA 835
QY 150 GTTTCATCTCTCGAGTCTAGTAAGAGTCTCCTGTATAGGATGGGACAGATCACTTG 209
Db 834 GCCTCAATCTCTCGAGGCCAGTCAGAGCCCTCTGTACAGTATGGAATATCTTATCTG 775
QY 210 AATGGTTTCTCGAGACAGCAGCAATCTCCTCAGCTCCTGATGATATTTGATGTCAC 269
Db 774 AATGGTACCTCGAGAGCCAGGACGCTCTCCAGGGCTGTATCTTCTGTTTCCAA 715
QY 270 CGTGCATCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTCA 329
Db 714 CGGACTCTGGGGTCCAGACAGGTTTCAGTGGCAGTGGGTGAGGACAGATTTTCA 655
QY 330 GAAATCAGTAGAGTGAAGGCTGAGGATGCTGGGTGTGTTTACTGTCAACAACTTTAG 389
Db 654 AGAATCAGAGGTTGGAGGCTGACGACCTCGGTGTTTATTACTGCGGTCAAGGTTTAC 595
QY 390 TATCCATTCAGTCTCGGCTCGGGGACAAAGTTGGAATAAAACGTA 435
Db 594 CATCCTCTCACTTTCGCGCCAGGTACCAAGCTGGAGATCAACCGGA 549

RESULT 6

US-09-479-614-23
; Sequence 23, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479, 614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0

```
; SEQ ID NO 23
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Felis catus
US-09-479-614-23

Query Match      54.6%; Score 238.4; DB 9; Length 726;
Best Local Similarity 74.8%; Pred. No. 1.2e-70;
Matches 299; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 36 ATGAGGTTCTCTGTTCAGTTTCTGGGGTCTATCTCTGATCTCTGGAGTCAGTGGG 95
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ATGAGGTTCCCTGCTAGCTCTCTGGAGTCTATCTCTGATCTCTGGAGTCAGTGGG 60
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 96 GATATTGTGATTAACCCAGGAGTAACTCTCCAAATCTCTGATCTCTGGAGATCAGTTTC 155
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GATATTGTGATGAGCAGAGCCCTCTGTCCCTGTCCGTACCCCTGGAGAGCCAGCCTCA 120
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 156 ATCTCTCTGAGGTTCTAGTAAGAGTCTCTCTGATTAAGGATGGGAGACATCTTGAATTGG 215
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 ATCTCTCTGAGGTTCTAGTAAGAGTCTCTCTGATTAAGGATGGGAGACATCTTGAATTGG 180
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 216 ATCTCTCTGAGGTTCTAGTAAGAGTCTCTCTGATTAAGGATGGGAGACATCTTGAATTGG 275
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 ATCTCTCTGAGGTTCTAGTAAGAGTCTCTCTGATTAAGGATGGGAGACATCTTGAATTGG 240
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 276 TCAGGAGTCTCAGACCCAGGAGTAACTCTCCAAATCTCTGATCTCTGGAGATCAGTTTC 335
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 TCAGGAGTCTCAGACCCAGGAGTAACTCTCCAAATCTCTGATCTCTGGAGATCAGTTTC 300
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 336 AGTAGAGTGAAGGCTGAGGATGTTGGGTGTGTTACTGTCAACAACACTTGTAGAGTATCCA 395
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 AGTAGAGTGAAGGCTGAGGATGTTGGGTGTGTTACTGTCAACAACACTTGTAGAGTATCCA 360
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 396 TTCACGTTTCGGCTCGGGGACAAAAGTTGGAAATAAAACGTA 435
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 CTCACCTTCGGCCCGAGGTACCAAGCTGGAGATCAAAACGGA 327
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 8
US-09-905-243-55
; Sequence 55, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Macaca cynomolgus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(399)
US-09-905-243-55

Query Match      51.2%; Score 223.6; DB 10; Length 399;
Best Local Similarity 72.6%; Pred. No. 9.4e-66;
Matches 289; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Qy 36 ATGAGGTTCTCTGTTCAGTTTCTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ATGAGGTTCCCTGCTAGCTCTCTGGGCTGCTATTGCTCTGCTCCCGGATCCAGTGGG 60
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 96 GATATTGTGATAACCCAGGATGAACCTCCCAATCTCTGATCTCTGGAGATCAGTTTC 155
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCTCTCCCTGGAGACCCCTCC 120
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 156 ATCTCTCTGAGGTTCTAGTAAGAGTCTCTCTGATTAAGGATGGGAGACATCTTGAATTGG 215
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 ATCTCTCTGAGGTTCTAGTAAGAGTCTCTCTGATTAAGGATGGGAGACATCTTGAATTGG 180
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 216 TTCCTGAGAGACCCAGGACATCTCTCAGCTCCCTGATGTTTATTCATCTTCAACCGGCAC 275
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TTACAACAGAGACCCAGGACATCTTCAAGACTCTCTGATTTATCAGGTTTCTTAAACCGGCAC 240
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 276 TCAGGAGTCTCAGACCCGGTTTATGTCAGTGGGTCAAGGACAGATTTTCAACCTCGAAATC 335
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 TCTGGGTCTCCAGACAGATTTCAAGGCTGGGCGGAGGACAGATTTCAACCTCGAAATC 300
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 336 AGTAGAGTGAAGGCTGAGGATGTTGGGTGTGTTACTGTCAACAACACTTGTAGAGTATCCA 395
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 AGTAGAGTGAAGGCTGAGGATGTTGGGTGTGTTACTGTCAACAACACTTGTAGAGTATCCA 360
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 396 TTCACGTTTCGGCTCGGGGACAAAAGTTGGAAATAAAACG 433
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```



```

; NAME/KEY: misc_feature<222> (1)..(420)
; OTHER INFORMATION: Sequence coding for the variable region of the antibody light chain
; OTHER INFORMATION: ain
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(57)
; OTHER INFORMATION:
US-09-341-894-3

```

Query Match	50.0%;	Score 218.6;	DB 9;	Length 420;
Best Local Similarity	73.7%;	Pred. No. 4.8e-64;		
Matches 278;	Conservative 0;	Mismatches 99;	Indels 0;	Gaps 0;
Qy 57	CTGGGGTGCTTATGTCTGGATCTCTGGAGTCTAGTGGGGATATTGTGATAACCCAGGAT	116		
Db				
Qy 19	CTGTTGGTGTATGTTCTGTGATTCCTGTCTCCAAATAGTAAATGTTGTGATGACCCAACT	78		
Db				
Qy 117	GAATCTCCAATCTGTCTCACTCTCTGGAGATCACTTTTCCATCTCCTCAGGTCTAGTAAG	176		
Db				
Qy 79	CCACTCTCCCTGTCTGTCTAGTCTTGGAGATCAAGCCCTCCATCTCTGCAGATCTAGTCAG	138		
Db				
Qy 177	AGTCTCCTGTATAGGATGGGAGACATACTTGAATTGGTTTCTGCAGAGACCAGGACAA	236		
Db				
Qy 139	AGCATGTACATAGTAAATGAAACACTATTTGAATGGTACCTGCAGAAACAGGCCAG	198		
Db				
Qy 237	TCCTCTCAGTCTCTGTATGTTGATGTCACACCGTGCATCAGGAGTCTCAGACCGGTTT	296		
Db				
Qy 199	TCCTCAAAGCTCTGTATTAAGTTTCCACCGATTGTCTGGGTCCCGACAGAGTTC	258		
Db				
Qy 297	AGTGGCAGTGGGTCCAGCACAGATTTACCCCTGGAATCAGTAGAGTGAGGCTGAGGAT	356		
Db				
Qy 259	AGTGGCAGTGGATCAGGGACAGACTTTCACACTCAAATCAGCAGATGTGAGGCTGAGGAT	318		
Db				
Qy 357	GTGGGTGTGTATTACTGTCAACAACCTGTGAGAGTATCCATTACGTTCCGGCTCGGGGACA	416		
Db				
Qy 319	CTGGGACTTTATTACTGTGTTTCAAGGTTCCATATTCATTCCGTTTCGGGTTCGGGGACA	378		
Db				
Qy 417	AAGTTGGAATAAAGC	433		
Db				
Qy 379	AAGTTGGAATAAAGC	395		
Db				

```

RESULT 12
US-10-060-036-3813
: Sequence 3813, Application US/10060036
: Publication No. US20030073144A1
: GENERAL INFORMATION:
: APPLICANT: Benson, Darin R.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Lodes, Michael J.
: APPLICANT: Persing, David H.
: APPLICANT: Hepler, William T.
: APPLICANT: Jjiang, Yugu
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
: FILE REFERENCE: 210121.566
: CURRENT APPLICATION NUMBER: US/10/060.036
: TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
: FILE REFERENCE: 22851-032
: CURRENT APPLICATION NUMBER: US/09/881.823
: CURRENT FILING DATE: 2001-06-15
: PRIOR APPLICATION NUMBER: US 07/378,577
: PRIOR FILING DATE: 1999-08-20
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 9
: LENGTH: 420
: TYPE: DNA
: ORGANISM: Murine
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (13)..(417)
US-09-881-823-9

```

```

; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3813
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 490
; OTHER INFORMATION: n = A,T,C or G
US-10-060-036-3813

Query Match          49.0%; Score 214; DB 10; Length 420;
Best Local Similarity 70.4%; Pred. No. 1.7e-62;
Matches 286; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 32 CACCATGAGTTCTCTGTCAGTTTCTGGGGTGCTTATGTTCTTGAGTCTCTGGAGTCAG 91
||||| | | | | | | | | | | | | | | | | |
Db 9 CACCATGATGACTCTGCCCCAGTTCCTGTTCTGTTAGTCTCTGGATCGGGAAACCAA 68

QY 92 TGGGATATTCTGATACCCAGGATGAACCTCTCCAATCTCTGTCACCTTCTGGAGAATCAGT 151
||| | | | | | | | | | | | | | | | |
Db 69 CGGTGATGTTCTGATGACCCAGACTCCCACTCACTTTCTCGGTTACCATTGGACAACAGC 128

QY 152 TTCCATCTCCTGCGAGGTCTAGTAGAGTCTCCCTGTATAGGATGGGAACATACTTTGA 211
||||| | | | | | | | | | | | | | | | | |
Db 129 CTCATCTCTTTGCAAGTCAAGTCAGAGCCCTCTTAGATCGTGTGGAAGGACATATTAG 188
||||| | | | | | | | | | | | | | | | | |

```



```
; LENGTH: 720 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..720
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..720
US-09-948-429B-5

Query Match      48.4%; Score 211.6; DB 9; Length 720;
Best Local Similarity 70.4%; Pred. No. 1.4e-61;
Matches 283; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

Qy 36 ATGAGGTTCTCTGTTCAGTTTCTGGGGTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95
Db 1 ATGAGCCTCCCTGTCTCAGCTCCTCGGGTCTGCTATTGCTCTGGTCCCGGGTCCAGTGGG 60

Qy 96 GATATTGTGATAACCCAGGATGAATCTCCAAATCCTGTCACTTCTGGAGAAATCAGTTTCC 155
Db 61 GAAATTGTGATGACTCAGTCTCCACTGTCCCTTCCCATCACACCTGGAGCCGGCCCTCC 120

Qy 156 ATCTCCTGCAGGTCTAGTAAGAGTCTCTGTATAGAGATGGGAAGACATCTTGAATTGG 215
Db 121 ATCTCCTGTAGTCTTAGTCAAGGCTTAAACACAGTAAATGGAGACACCTTCTCTGAGTTGG 180

Qy 216 TTTCTGCAGAGACCAGGACAATCTCCTCAGCTCCTGATGATTTGATGTCACCCGTGCA 275
Db 181 TATCAGCAGAGCCAGGCCAACCTCCRAGGCTCCTGATTTATAAGGTTTCTAACCCGGAC 240

Qy 276 TCAGAGTCTCAGACCCGGTTTGTGGAGTGGGTGAGGCACAGATTTACCCCTGGAATC 335
Db 241 TCTGGGTCCAGACAGATTCAGGGGAGTGGGGCAGGACAGATTTACACTGAAATC 300

Qy 336 AGTAGAGTGAAGGCTGAGAGTGTGGGTGTGTTACTGTCAACAACCTGTAGAGTATCCA 395
Db 301 AGCGCAGTGGAGGCTGAGAGTGTGGGTGTTTCTGCGGGCAAGGTACAAGACTCCT 360

Qy 396 TTCAGGTTCCGCTCGGGACAAAGTTGGAATAAAACGTACG 437
Db 361 CCCACTTTCGGCGGAGGACCAAGGTGGAATCAAACGTACG 402
```

Search completed: April 26, 2003, 09:24:09
Job time : 47.2347 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:57:16 ; Search time 18,1006 seconds
(without alignments)
7404.053 Million cell updates/sec

Title: US-09-674-716B-2
Perfect score: 437
Sequence: 1 agctttacagtactcagc.....agttggaataaacgtagc 437

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCIRUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	317.2	72.6	339	2	US-08-672-345C-88
2	317.2	72.6	339	4	US-09-214-095D-99
3	317.2	72.6	368	2	US-08-672-345C-86
4	317.2	72.6	368	4	US-09-214-095D-107
5	316	72.3	420	4	US-09-214-095D-111
6	309.2	70.8	368	2	US-08-672-345C-90
7	309.2	70.8	368	4	US-09-214-095D-103
8	293.2	67.1	464	1	US-08-438-123-15
9	276.4	63.2	399	1	US-08-253-877C-9
10	276.4	63.2	399	2	US-08-452-164A-9
11	276.4	63.2	396	3	US-08-603-024-3
12	249.6	57.1	336	3	US-08-483-749A-3
13	248.4	56.8	339	4	US-09-406-532-13
14	240	54.9	882	1	US-08-392-419-3
15	236	54.0	373	3	US-08-732-708C-40
16	230.8	52.8	1095	3	US-08-875-811-52
17	230.8	52.8	1098	3	US-08-875-811-54
18	226.2	51.8	405	1	US-08-259-372A-11
19	226.2	51.8	405	1	US-08-468-671-11
20	223.6	51.2	427	1	US-08-053-171-8
21	221.4	50.7	325	1	US-08-468-661-4
22	221.4	50.7	325	1	US-08-466-272A-4
23	221.4	50.7	325	1	US-08-478-857-4
24	221.4	50.7	325	2	US-08-471-771-4
25	221.4	50.7	325	3	US-09-130-783-4
26	219	50.1	434	1	US-08-053-171-4
27	212.8	48.7	394	1	US-08-129-930B-93

28	212.8	48.7	394	4	US-08-134-346A-48	Sequence 48, Appl
29	212.8	48.7	394	4	US-08-976-288A-93	Sequence 93, Appl
30	211.6	48.4	720	3	US-08-487-550-5	Sequence 5, Appl
31	211.2	48.3	394	1	US-07-977-696C-64	Sequence 64, Appl
32	211.2	48.3	394	1	US-08-129-930B-64	Sequence 64, Appl
33	211.2	48.3	394	4	US-08-976-288A-64	Sequence 64, Appl
34	206.6	47.3	424	3	US-08-589-939-8	Sequence 8, Appl
35	206.6	47.3	537	5	PCT-US91-02942-2	Sequence 2, Appl
36	206.6	47.3	537	5	PCT-US91-02946-2	Sequence 2, Appl
37	206.4	47.2	394	1	US-07-977-696C-26	Sequence 26, Appl
38	206.4	47.2	394	1	US-08-129-930B-26	Sequence 26, Appl
39	206.4	47.2	394	4	US-08-134-346A-13	Sequence 13, Appl
40	206.4	47.2	394	4	US-08-976-288A-26	Sequence 26, Appl
41	206.2	47.2	339	1	US-08-264-093-9	Sequence 9, Appl
42	205.8	47.1	714	3	US-09-192-545-3	Sequence 3, Appl
43	205	46.9	384	1	US-08-482-882-44	Sequence 44, Appl
44	205	46.9	384	1	US-08-483-389-44	Sequence 44, Appl
45	205	46.9	384	2	US-08-487-113D-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-08-672-345C-88
; Sequence 88, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-672-345C-88

Query Match 72.6%; Score 317.2; DB 2; Length 339;
Best Local Similarity 96.2%; Pred. No. 7.8e-97;
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 96 GATATTGTGTAACCCAGGATGAACCTCCAACTCTCTGAGAAATCAGTTTCC 155
Db 1 GATATTGTGATGACCCAGGATGAACCTCCAACTCTCTGAGAAATCAGTTTCC 60
Qy 156 ATCTCTTCGAGGTCTCTGTAAGAGTCTCTGTATAGAGTGGAGAGACATCTGTAATTGG 215

Db 61 ATCTCTCGAGGCTAGTAGGAGTCTCTATATAGGAGTGGGAAGACATACCTTGAATTGG 120
QY 216 TTTCTGCAGACAGGACAAATCTCTCAGCTCCTGATGTTATTTGATGTCACCCGTGCA 275
Db 121 TTTCTGCAGACAGGACAGATCTCTCAACTCTGATCTATTTGATGTCACCCGTTC 180
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGCACAGATTTTACCCCTGGAATC 335
Db 181 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGAACAGATTTTACCCCTGGAATC 240
QY 336 AGTAGAGTGAAGGCTGAGGATCTGGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA 395
Db 241 AGTAGAGTGAAGGCTGAGGATCTGGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA 300
QY 396 TTCAGGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433
Db 301 TTCAGGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 338

RESULT 2

US-09-214-095D-99
; Sequence 99, Application US/09214095D

; Patent No. 6280987

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214, 095D

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 99

; LENGTH: 339

; TYPE: DNA

; ORGANISM: Murline

US-09-214-095D-99

Query Match 72.6%; Score 317.2; DB 4; Length 339;
Best Local Similarity 96.2%; Pred. No. 7.8e-97;
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTGATAACCCAGGATGAACCTCCAAATCCTGTCACTTCTTGAGAAATCAGTTTCC 155
Db 1 GATATTGTGATGACCAAGACAGCAACTCTCCAATCCTGTCACTTCTTGAGAAATCAGTTTCC 60
QY 156 ATCTCTCGAGGCTAGTAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATTGG 215
Db 61 ATCTCTCGAGGCTAGTAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATTGG 120
QY 216 TTTCTGCAGACAGGACAAATCTCTCAGCTCCTGATGTTATTTGATGTCACCCGTGCA 275
Db 121 TTTCTGCAGACAGGACAGATCTCTCAACTCTGATCTATTTGATGTCACCCGTTC 180
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGCACAGATTTTACCCCTGGAATC 335
Db 181 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGAACAGATTTTACCCCTGGAATC 240
QY 336 AGTAGAGTGAAGGCTGAGGATCTGGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA 395
Db 241 AGTAGAGTGAAGGCTGAGGATCTGGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA 300
QY 396 TTCAGGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433
Db 301 TTCAGGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 338

RESULT 3

US-08-672-345C-86

; Sequence 86, Application US/08672345C

; Patent No. 5948658

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald, W.

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-672-345C-86

Query Match 72.6%; Score 317.2; DB 2; Length 368;
Best Local Similarity 96.2%; Pred. No. 8.1e-97;

Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTGATAACCCAGGATGAACCTCCAAATCCTGTCACTTCTTGAGAAATCAGTTTCC 155
Db 1 GATATTGTGATGACCAAGACAGCAACTCTCCAATCCTGTCACTTCTTGAGAAATCAGTTTCC 60
QY 156 ATCTCTCGAGGCTAGTAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATTGG 215
Db 61 ATCTCTCGAGGCTAGTAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATTGG 120
QY 216 TTTCTGCAGACAGGACAAATCTCTCAGCTCCTGATGTTATTTGATGTCACCCGTGCA 275
Db 121 TTTCTGCAGACAGGACAAATCTCTCACTCTCTGATCTATTTGATGTCACCCGTGCA 180
QY 276 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGCACAGATTTTACCCCTGGAATC 335
Db 181 TCAGGAGTCTCAGACCGGTTTGTAGTGGCAGTGGTTCAGGAACAGATTTTACCCCTGGAATC 240
QY 336 AGTAGAGTGAAGGCTGAGGATCTGGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA 395
Db 241 AGTAGAGTGAAGGCTGAGGATCTGGGTGTGTTACTGTCAACAACTTGTAGAGTATCCA 300
QY 396 TTCAGGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433
Db 301 TTCAGGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 338

RESULT 4

US-09-214-095D-107

; Sequence 107, Application US/09214095D

; Patent No. 6280987

; GENERAL INFORMATION:

; APPLICANT: Landry, Donald

; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

; FILE REFERENCE: 51400-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/214, 095D

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 121

```
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 368
; TYPE: DNA
; ORGANISM: Murine
US-09-214-095D-107

Query Match          72.6%; Score 317.2; DB 4; Length 368;
Best Local Similarity 96.2%; Pred. No. 8.1e-97;
Matches 325; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 96 GATATTGTGATAACCCAGGATGAACCTCCAAATCCTGTCACTTCTGGAGAATCAGTTTC 155
DB 1 GATATGGTGATGACGCAAGACAACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTC 60

QY 156 ATCTCCCTGCAGGCTAGTAGAGTCTCCTGTATAGAAGATGGGAGACATATCTTGAATTGG 215
DB 61 ATCTCCCTGCAGGCTAGTAGAGTCTCCTGTATAGAAGATGGGAGACATATCTTGAATTGG 120

QY 216 TTCTTCGAGACAGCAGCAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCCGTGCA 275
DB 121 TTCTTCGAGACAGCAGCAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCCGTGCA 180

QY 276 TCAGAGTCTCAGACCCGCTTAGTGCGAGTGGGTGCGGACAGATTTACCCCTGGAAATC 335
DB 181 TCAGAGTCTCAGACCCGCTTAGTGCGAGTGGGTGCGGACAGATTTACCCCTGGAAATC 240

QY 336 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGATTTACTGTCAACAACCTGTAGAGTATCCA 395
DB 241 AGTAGAGTGAAGGCTGAGGATGTGGGTGTGATTTACTGTCAACAATTTGTAGAGTATCCA 300

QY 396 TTCAGGTCGCGCTCGGGACAAAGTTGGAATAAAGC 433
DB 301 TTCAGGTCGCGCTCGGGACAAAGTTGGAATAAAGC 338

RESULT 5
US-09-214-095D-111
; Sequence 111, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 111
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: V_segment
; LOCATION: (1)..(403)
; OTHER INFORMATION: n at any position represents any nucleotide including c,g,t,a,u
US-09-214-095D-111

Query Match          72.3%; Score 316; DB 4; Length 420;
Best Local Similarity 95.6%; Pred. No. 2.2e-96;
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 94 GGGATATTGTGATAACCCAGGATGAACCTCCAAATCCTGTCACTTCTGGAGAATCAGTTT 153
DB 51 GCGATATGGTGATGACGCAAGATGAACCTCCAAATCCTGTCACTTCTGGAGAATCAGTTT 110

QY 154 CCATCTCCCTGCAGGCTAGTAGAGTCTCCTGTATAGAAGATGGGAGACATATCTTGAATT 213
DB 111 CCATCTCCCTGCAGGCTAGTAGAGTCTCCTGTATAGAAGATGGGAGACATATCTTGAATT 170

QY 214 GGTTCCTGCAGACAGCAGCAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCCGTG 273
DB 171 GGTTCCTGCAGACAGCAGCAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCCGTG 230
```

```
QY 274 CATCAGGACTCTCAGACCGGTTTAGTGCAGTGGGTGAGGACACAGATTTACCCCTGGAAA 333
DB 231 CATCAGGACTCTCAGACCGGTTTAGTGCAGTGGGTGAGGACACAGATTTACCCCTGGAAA 290

QY 334 TCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGATTTACTGTCAACAACCTGTAGAGTATC 393
DB 291 TCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGATTTACTGTCAACACATTTGTAGACTATC 350

QY 394 CATTCACGTTCCGGCTCGGGGACAAAGTTGGAATAAAGC 433
DB 351 CATTCACGTTCCGGCTCGGGGACAAAGTTGGAATAAAGC 390

RESULT 6
US-08-672-345C-90
; Sequence 90, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-672-345C-90
```

```
Query Match          70.8%; Score 309.2; DB 2; Length 368;
Best Local Similarity 94.7%; Pred. No. 3.9e-94;
Matches 320; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 96 GATATTGTGATAACCCAGGATGAACCTCCAAATCCTGTCACTTCTGGAGAATCAGTTTC 155
DB 1 GATATGGTGATGACGCAAGATGAACCTCCAAATCCTGTCACTTCTGGAGAATCAGTTTC 60

QY 156 ATCTCCCTGCAGGCTAGTAGAGTCTCCTGTATAGAAGATGGGAGACATATCTTGAATTGG 215
DB 61 ATCTCCCTGCAGGCTAGTAGAGTCTCCTGTATAGAAGATGGGAGACATATCTTGAATTGG 120

QY 216 TTCTTCGAGACAGCAGCAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCCGTGCA 275
DB 121 TTCTTCGAGACAGCAGCAATCTCCTCAGCTCCTGATGTATTTGATGTCCACCCGTGCA 180

QY 276 TCAGAGTCTCAGACCCGCTTAGTGCGAGTGGGTGCGGACAGATTTACCCCTGGAAATC 335
DB 181 TCAGAGTCTCAGACCCGCTTAGTGCGAGTGGGTGCGGACAGATTTACCCCTGGAAATC 240
```

QY 336 AGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACAACCTGTGTAGAGTATCCA 395
Db 241 AGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACAACCTGTGTAGAGTATCCA 300
QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAAATAAAACG 433
Db 301 TTCACGTTCCGGCTCGGGGACAAATTTGGAGATAAAACG 338

RESULT 7

US-09-214-095D-103
; Sequence 103, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 103
; LENGTH: 368
; TYPE: DNA
; ORGANISM: MURINE
US-09-214-095D-103

Query Match 70.8%; Score 309.2; DB 4; Length 368;
Best Local Similarity 94.7%; Pred. No. 3.9e-94;
Matches 320; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 96 GATATTGTGATACCAACCGAGTGAACCTCTCCAATCCTGTGACATCTCTGGAGAATCAGTTTCC 155
Db 1 GATATGGTGATGACGCAAGATGAACCTCTCCAATCCTGTGACATCTCTGGAGAATCAGTTTCC 60
QY 156 ATCTCTGCAGGCTCTAGTAGAGTCTCCGTGTATAGGATGGGAACATACCTTGAATTGG 215
Db 61 ATCTCTGCAGGCTCTAGTAGAGTCTCCGTGTATAGGATGGGAACATACCTTGAATTGG 120
QY 216 TTTCTGCAGAGACGAGCAAAATCTCCTCAGCTCCTGTATTTGATGTCCACCCGTCGA 275
Db 121 TTTCTGCAGAGACGAGCAAAATCTCCTCAGCTCCTGTATTTGATGTCCACCCGTCGA 180
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGCAGTGGGTGAGGACAGATTTTCAACCTGGAAATC 335
Db 181 TCAGGAGTCTCAGACCGGTTTAGTGCAGTGGGTGAGGACAGATTTTCAACCTGGAAATC 240
QY 336 AGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACAACCTGTGTAGAGTATCCA 395
Db 241 AGTAGAGTGAAGCTGAGGATGGGTGTGTATTACTGTCAACAACCTGTGTAGAGTATCCA 300
QY 396 TTCACGTTCCGGCTCGGGGACAAAGTTGGAAATAAAACG 433
Db 301 TTCACGTTCCGGCTCGGGGACAAATTTGGAGATAAAACG 338

RESULT 8

US-08-438-123-15
; Sequence 15, Application US/08438123
; Patent No. 5532293
; GENERAL INFORMATION:
; APPLICANT: Lindholm et al
; TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,123
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/906,350
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: J.G. Mullins
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 149-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-438-123-15
Query Match 67.1%; Score 293.2; DB 1; Length 464;
Best Local Similarity 82.2%; Pred. No. 1e-88;
Matches 337; Conservative 0; Mismatches 73; Indels 0; Gaps 0;
QY 24 CAGGACCTCACCATGAGGTTCTCTGTTCAGTTTCTGGGGGTGCTTATGTTCTGGATCTCT 83
Db 30 CAAGTTCTCAGAATGAGTGCCTAGCTAGTTCCTCGGGGCTGCTTGTGCTCTGGATCCTCT 89
QY 84 GGAGTCAGTGGGGATATTGTGATAACCCAGAGTGAACCTCTCCAATCCTGTCACTTCTGGA 143
Db 90 GGAGTCAGTGGGGATATTGTGATAACCCAGAGTGAACCTCTCCAATCCTGTCACTTCTGGA 149
QY 144 GAATCAGTTTCCATCTCTGCGAGGCTCTAGTAAGAGTCTCTCTGTATAGAGTGGGAAGACA 203
Db 150 GAGTCAGTATCCATCTCTGCGAGGCTCTAGTAAGAGTCTCTCTGTATAGAGTGGGAAGACA 209
QY 204 TACTTCAATTTGGTTTCTGCGAGAGCCAGGACAAATCTCTCAGCTCCTGATGTTATTTGATG 263
Db 210 TACTTGTATTTGGTTTCTGCGAGAGCCAGGACCTCTCTCAGCTCCTGATATATCGGATG 269
QY 264 TCACCCGCTGCATCTCAGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTTC 323
Db 270 TCCAACTTTGTTCTCAGGAGTCCCGACAGAGTTTCAAGTGGGTCAGGAGTCTGCTTTC 329
QY 324 ACCTCGAATCAGTAGAGTGAAGGCTGAGGATGTTAGTGGCAGTGGGTGAGGACAGATTTTC 383
Db 330 ACATGAGATCAGTAGAGTGGAGGCTGAGGATGTTAGTGGGTTTATTTACTGTCAACAACCT 389
QY 384 GTAGAGTATCCATTTACGTTTCGGCTCGGGGACAAAGTTGGAAATAAAACG 433
Db 390 CTAGAGTATCCGTTTCAAGTTTCTGCTCGGACCAAGTGGAGCTGAAACG 439

RESULT 9
US-08-253-877C-9
; Sequence 9, Application US/08253877C
; Patent No. 5773001
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methylthio Antitumor
; Agents and Intermediates for Their Synthesis

```
;
;
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470-8426
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..399
;
; US-08-253-877C-9
```

```
Query Match 63.2%; Score 276.4; DB 1; Length 399;
Best Local Similarity 80.9%; Pred. No. 4e-83;
Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTTCAGTTTCTGGGGTGCCTTATGTTCTGATCTCTGGAGTCAGTGGG 95
DB 1 ATGAGGTGCTTAGCTAGTTCTGTTGGGGTGCCTGTTGCTCTGGATCCCTGGAGCCATTGGG 60

QY 96 GATATTGTGATAACCCAGGATGAACCTCCAACTCTGTCACCTCTGGAGAAATCAGTTTCC 155
DB 61 GATATTGTGATGACTCAGGCTGCACCCCTCTCTCTGCTCACTCTCTGGAGAGTCATTATCC 120

QY 156 ATCTCTCCAGGCTAGTAAGAGTCTCTCTATAGAGTGGGAGACATATCTTCAATTGG 215
DB 121 ATTTCTCGAGGCTAGTAAGAGTCTCTCTATAGTAAATGGCGACACTTTCTTGTATTGG 180

QY 216 TTCTGCGAGAGCAGGACAACTCTCTCAGCTCCTGATGATATTTGATGTCACCCGTGCA 275
DB 181 TTCTGCGAGAGCCAGGCGCAGTCTCTCTCACTCTGATATATCGGATGTCACACTTGGC 240

QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACACAGATTTACCCCTGGAATC 335
DB 241 TCCGGAGTCCCGACAGGCTTCCAGTGGCAGTGGGTTCAGTGGGTCAGGAACTGCTTTCACATGAGAGTC 300

QY 336 AGTAGAGTGAAGGCTGAGGATGTTGGGTGTGTAFTACTGTCAACAACCTGTAGAGATATCCA 395
DB 301 AGTAGAGTGGAGCTGAGGATGTTGGGTGTTATTACTGTATGCAACATCTAGAATATCCT 360

QY 396 TTACGTTTGGGCTGGGGACAAAGTTGGAAATAAAGC 433
DB 361 TTCAGGTTCTGGTCTGGGACCAAGCTGGAGCTGAAACG 398
```

RESULT 10

US-08-452-164A-9

; Sequence 9, Application US/08452164A

; Patent No. 5877296

```
;
;
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,164A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..399
;
; US-08-452-164A-9
```

```
Query Match 63.2%; Score 276.4; DB 2; Length 399;
Best Local Similarity 80.9%; Pred. No. 4e-83;
Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 36 ATGAGGTTCTCTGTTTCAGTTTCTGGGGTGCCTTATGTTCTGATCTCTGGAGTCAGTGGG 95
DB 1 ATGAGGTGCTTAGCTAGTTCTGTTGGGGTGCCTGTTGCTCTGGATCCCTGGAGCCATTGGG 60

QY 96 GATATTGTGATAACCCAGGATGAACCTCCAACTCTGTCACCTCTGGAGAAATCAGTTTCC 155
DB 61 GATATTGTGATGACTCAGGCTGCACCCCTCTCTCTGCTCACTCTCTGGAGAGTCATTATCC 120

QY 156 ATCTCTCCAGGCTAGTAAGAGTCTCTCTATAGAGTGGGAGACATATCTTCAATTGG 215
DB 121 ATTTCTCGAGGCTAGTAAGAGTCTCTCTATAGTAAATGGCGACACTTTCTTGTATTGG 180

QY 216 TTCTGCGAGAGCAGGACAACTCTCTCAGCTCCTGATGATATTTGATGTCACCCGTGCA 275
DB 181 TTCTGCGAGAGCCAGGCGCAGTCTCTCTCACTCTGATATATCGGATGTCACACTTGGC 240

QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACACAGATTTACCCCTGGAATC 335
DB 241 TCCGGAGTCCCGACAGGCTTCCAGTGGCAGTGGGTTCAGTGGGTCAGGAACTGCTTTCACACTGAGAGTC 300

QY 336 AGTAGAGTGAAGGCTGAGGATGTTGGGTGTGTAFTACTGTCAACAACCTGTAGAGATATCCA 395
DB 301 AGTAGAGTGGAGCTGAGGATGTTGGGTGTTATTACTGTATGCAACATCTAGAATATCCT 360
```

QY 396 TTCAGGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433
|||||
Db 361 TTCAGGTTCCGCTCGGGGACCAAGCTGGAGCTGAAACG 398
|||||
RESULT 11
US-08-603-024-3
; Sequence 3, Application US/08603024
; Patent No. 6015562
; GENERAL INFORMATION:
; APPLICANT: Himman, Lois M.
; APPLICANT: Menendez, Ana T.
; APPLICANT: Hamann, Philip R.
; TITLE OF INVENTION: TARGETED FORMS OF METHYLTRITHIO
; TITLE OF INVENTION: ANTITUMOR AGENTS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: NJ
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/603,024
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,932-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-683-2158
; TELEFAX: 973-683-4117
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..399
US-08-603-024-3

Query Match 63.2%; Score 276.4; DB 3; Length 399;
Best Local Similarity 80.9%; Pred. No. 4e-83;
Matches 322; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 36 ATGAGGTTCTCTGCTCAGTTCTCGGGGCTCTTATGTTCTGGATCTCTGGAGTCAGTGGG 95
|||||
Db 1 ATGAGGTCCTAGCTGAGTTCTCGGGGCTCTTGTGCTCTGGATCTCTGGAGCCATTGGG 60
|||||
QY 96 GATATTGTGATAACCCAGGATGAACCTCTCCAATCCTGTCACTTCTGGAGATCAGTTTCC 155
|||||
Db 61 GATATTGTGATGACTCAGGCTGACCCCTCTGTCCTGTCACTCTCTGGAGATCATTATCC 120
|||||
QY 156 ATCTCCGTCAGGCTCTAGTAAGAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 215
|||||
Db 121 ATTTCTGTCAGGCTCTAGTAAGAGTCTCTCTCATAGTAATAGGCGACACTTCTTGTATTGG 180
|||||
QY 216 TTCTGTCAGAGCCAGGACCAATCTCTCAGCTCTCTGATGTTGATGTCACCCCGTGA 275
|||||
Db 181 TTCTGTCAGAGGCGGCGCCAGTCTCTCAACTCTCTGATATGCGGATGTCACACCTTGGC 240
|||||
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTCCACCTTGGAAATC 335
|||||

Db 241 TCCGAGTCCAGACAGGTTCACTGGCAGTGGGTGAGGAACCTGCTTCACACTGAGAGTC 300
|||||
QY 336 AGTAGAGTGAAGGCTCAGGATGTGGGTGTATTACTGTCAACAACACTTGTAGAGTATCCA 395
|||||
Db 301 AGTAGAGTGGAGGCTGAGGATGTGGGTGTTTATTACTGTATGCAACATCTAGAAATATCCT 360
|||||
QY 396 TTCACGTTCCGCTCGGGGACAAAGTTGGAATAAAACG 433
|||||
Db 361 TTCACGTTCCGCTCGGGGACCAAGCTGGAGCTGAAACG 398
|||||
RESULT 12
US-08-483-749A-3
; Sequence 3, Application US/08483749A
; Patent No. 6054561
; GENERAL INFORMATION:
; APPLICANT: RING, DAVID B.
; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
; CITY: EMERYVILLE
; STATE: CA
; COUNTRY: USA
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,749A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SAVERIDE, PAUL B.
; REGISTRATION NUMBER: 36,914
; REFERENCE/DOCKET NUMBER: 0508.008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2585
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..336
US-08-483-749A-3

Query Match 57.1%; Score 249.6; DB 3; Length 336;
Best Local Similarity 83.9%; Pred. No. 3.5e-74;
Matches 282; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
QY 96 GATATTGTGATAACCCAGGATGAACCTCTCCAATCCTGTCACTTCTGGAGATCAGTTTCC 155
|||||
Db 1 GATATTGTGATGACCAAGCAGCAGCCCTCTGTACTGTCACTCTCTGGAGATCAGTATCC 60
|||||
QY 156 ATCTCCTCAGGCTCTAGTAAGAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 215
|||||
Db 61 ATCTCCTCAGGCTCTAGTAAGAGTCTCTGTATAGTAAATGCAACACTTCTTGTATTGG 120
|||||
QY 216 TTCTGTCAGAGCCAGGACCAATCTCTCAGCTCTCTGATGTTGATGTCACCCCGTGA 275
|||||
Db 121 TTCTGTCAGAGGCGGCGCCAGTCTCTCAGCTCTCTGATATATCGGATGTCACACCTTGGC 180
|||||
QY 276 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGGACAGATTTCCACCTTGGAAATC 335
|||||

Db 181 TCAGGAGTCCACAGAGTTCACTGCGAGTGGTCAAGAACTCTTTCACACTGACAATC 240
QY 336 AGTAGAGTGAAGCTGAGGATGTTGGGTGCTATTACTGTCAACAACACTTAGAGTATCCA 395
Db 241 AGTAGAGTGAAGCTGAGGATGTTGGGTGCTATTACTGTCAACAACACTTAGAGTATCCA 300
QY 396 TTCACGTTCCGCTCGGGGCAAAAGTTGGGAATAAAA 431
Db 301 TTCACGTTCCGCTCGGGGCAAAAGTTGGGAATAAAA 336

RESULT 13
US-09-406-532-13
; Sequence 13, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: Tie2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(339)
; OTHER INFORMATION: 13H10 light chain v region
US-09-406-532-13

Query Match 56.8%; Score 248.4; DB 4; Length 339;
Best Local Similarity 83.4%; Pred. No. 8.8e-74;
Matches 282; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 96 GATATTGTGTAACCCAGGATGAACCTCCAACTCTGCTACCTTCTGGAGAACTAGTTCC 155
Db 1 GATATCGTGATGACTCAGGCTGCATCTCTGTACCTGTCTGCTGAGAGTCACTATCC 60

QY 156 ATCTCTCCAGCTCTAGTAAGAGTCTCTGTATAGAGTGGGAAGACATCTTCAATTGG 215
Db 61 ATCTCTCCAGCTCTAGTAAGAGTCTCTGTATAGAGTGGGAAGACATCTTCAATTGG 120

QY 216 TTCTCTGCAGACCCAGGACAACTCTCTCAGCTCTCTGATGATTTGATGTCACCCGTCGA 275
Db 121 TTCTCTGCAGACCCAGGACAACTCTCTCAGCTCTCTGATGATTTGATGTCACCCGTCGA 180

QY 276 TCAGAGTCTCAGACCGTTTGTAGTGGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 335
Db 181 TCAGAGTCTCAGACCGTTTGTAGTGGCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240

QY 336 AGTAGAGTGAAGCTGAGGATGTTGGGTGCTATTACTGTCAACAACACTTAGAGTATCCA 395
Db 241 AGTAGAGTGAAGCTGAGGATGTTGGGTGCTATTACTGTCAACAACACTTAGAGTATCCA 300

QY 396 TTCACGTTCCGCTCGGGGCAAAAGTTGGGAATAAAA 433
Db 301 TTCACGTTCCGCTCGGGGCAAAAGTTGGGAATAAAA 336

RESULT 14
US-08-392-419-3
; Sequence 3, Application US/08392419
; Patent No. 5624659
; GENERAL INFORMATION:
; APPLICANT: Bigner, Darell D.
; APPLICANT: Zelutsky, Michael R.

; TITLE OF INVENTION: METHOD OF TREATMENT
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 5624659th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,419
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/033,827
; FILING DATE: 19-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5405-90
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 882 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(121..168, 527..874)
US-08-392-419-3

Query Match 54.9%; Score 240; DB 1; Length 882;
Best Local Similarity 79.2%; Pred. No. 9.1e-71;
Matches 285; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 78 ATCTCTGAGTCACTGGGATATTGTGATAACCCAGGATGAACCTCTCCAACTCTGTCAC 137
Db 521 ATTGAGGATCCCACTGCAGATATTGTGATGACGAGGCTGCATTTCCCAATCCAGTCA 580

QY 138 TCTGGAGAACTCACTTCCATCTCTCAGGCTCTAGTAAGAGTCTCTCTGTATAGGATGG 197
Db 581 CTGGGAACATCACTGCTCCATCTCTCTGAGGCTCTAGTAAGAGTCTCTCTACATAGTATGG 640

QY 198 AAGACATATCTTGAATTTGTTCTGCAGAGACAGGACAAATCTCTCAGCTCTGATGTAT 257
Db 641 ATCATTTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 700

QY 258 TTGATGTCCACCGTGCATCAGAGTCTCAGACCGTTTGTAGTGGTGGTGGTGGTGGTGG 317
Db 701 CAGATGTCCCACTGCTCTCAGGATCCCAAGAGTTCAGTAGCAGTGGGTGGGTGGTGG 760

QY 318 GATTTCACCTTGGAAATCAGTAGAGTGAAGCTGAGGATGTTGTTGTTGTTGTTGTTGTTG 377
Db 761 GATTTCACCTTGGAAATCAGTAGAGTGAAGCTGAGGATGTTGTTGTTGTTGTTGTTGTTG 820

QY 378 CAACCTGTAGAGTATCCATTCACGCTTCGGGTTCGGGGACAAAGTTGGAATAAATACGTAC 437
Db 821 CAAATCTAGAACTTCTCTCGGACCTTCGGTGGAGGCCAACCAAGCTGGAATAAATACGTAC 880

RESULT 15
US-08-732-708C-40
; Sequence 40, Application US/08732708C
; Patent No. 6127524

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:53:31 ; Search time 694.49 Seconds
(without alignments)
14583.043 Million cell updates/sec

Title: US-09-674-716b-17
Perfect score: 348
Sequence: 1 gatattgtgactcagtc.....agatcaaacgtacggtggct 348

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg_hum.*
31: em.htg_inv.*
32: em.htg_other.*
33: em.htg_mus.*
34: em.htg_pln.*
35: em.htg_rpd.*
36: em.htg_mam.*
37: em.htg_vrt.*
38: em.sy.*
39: em.htgo_hum.*
40: em.htgo_mus.*
41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	348	100.0	348	6	AX010614	AX010614 Sequence
c	348	100.0	348	6	AX010645	AX010645 Sequence
2	292	83.9	740	6	AX076853	AX076853 Sequence
c	292	83.9	740	6	AX076855	AX076855 Sequence
3	277.6	79.8	410	9	HSIGKLV46	X72467 H.sapiens m
4	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
5	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
6	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
7	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
8	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
9	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
10	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
11	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
12	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
13	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
14	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
15	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
16	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
17	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
18	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
19	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
20	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
21	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
22	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
23	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
24	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
25	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
26	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
27	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
28	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
29	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
30	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
31	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
32	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
33	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
34	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
35	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
36	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
37	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
38	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
39	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
40	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
41	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
42	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
43	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
44	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi
45	276	79.3	353	9	HSIGKLV46	AJ272080 Homo sapi

ALIGNMENTS

RESULT 1	AX010614	AX010614	348 bp	DNA	linear	PAT 06-SEP-2000
LOCUS	AX010614	Sequence 17 from Patent WO9558679.				
DEFINITION	AX010614	Sequence 17 from Patent WO9558679.				
ACCESSION	AX010614	Sequence 17 from Patent WO9558679.				
VERSION	AX010614.1	GI:9997425				
KEYWORDS		synthetic construct.				
SOURCE		artificial sequences.				
ORGANISM		1 (bases 1 to 348)				
REFERENCE		Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.				
AUTHORS		Antibodies to cd23, derivatives thereof, and their therapeutic uses				
TITLE		Patent: WO 9558679-A 17 18-NOV-1999;				
JOURNAL		BONNEFOY JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON				

BASE COUNT	81 a	87 c	97 g	83 t
ORIGIN				
	/note="Humanised anti-CD23 antibody light chain variable region" <1>248 /note="unnamed protein product" /codon_start=1 /transl_table=11 /protein_id="CAC07533.1" /db_xref="GI:9937426" /translation="DIVMTQSPISLPTVTPGPASISGRSSKSLLYKDGKTYLWYLQK PGPSPQLLIYLMSTRASGVDPDRFSGSGSGTDFTLKISRVEADVGYYVCOQLVEYFPT FGGGTGVEIKRTVA" 81 a 87 c 97 g 83 t			
CDS	/note="Humanised anti-CD23 antibody light chain variable region" <1>248 /note="unnamed protein product" /codon_start=1 /transl_table=11 /protein_id="CAC07533.1" /db_xref="GI:9937426" /translation="DIVMTQSPISLPTVTPGPASISGRSSKSLLYKDGKTYLWYLQK PGPSPQLLIYLMSTRASGVDPDRFSGSGSGTDFTLKISRVEADVGYYVCOQLVEYFPT FGGGTGVEIKRTVA" 81 a 87 c 97 g 83 t			

Db	168	TCAGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGCACAGATTTTACACTGAAATC	109
QY	241	AGCAGAGTGGAGGCTGAGGATGTTGGGCTTTATTACTGTCAACAGCTGGTAGAGTATCCA	300
Db	108	AGCAGAGTGGAGGCTGAGGATGTTGGGCTTTATTACTGTCAACAGCTGGTAGAGTATCCA	49
QY	301	TTCAACCTTCGGCCAGGGACCAAGGTGGAGATCAAACTACGGTGGCT	348
Db	48	TTCAACGTTTCGGCCAGGGACCAAGGTGGAGATCAAACTACGGTGGCT	1

```

1. .740
/organism="synthetic construct"
/db_xref="taxon:32630"
24. .740
/note="Synthetic sequence"
/codon_start=1
/transl_table=11
/protein_id="CAC32380.1"
/db_xref="GI:13121525"
/translation="MGWSCIILFLVATATGVHSDIVMTQSPLSLPVPMPGEPAISCRS
SKLLNSNGTYLYWLYLOKPGOSPOLLYOMNSLASGVDPRESSGSGCTOFTLKISR
EAEADVGVYCAOMLELIPRTFGGTKEIKRTVAASGVIFPPPSDEQKSGTASVYIC
NNYPPREAKVQMKVDAALPSQSGVSEVTEQDSKDSYSLSLSTLTLSKADYEHKKHYAC
EVTHQGLSSPVTKSPFRNGC"
187 a 201 c 165 t
BASE COUNT

```

Query Match 83.9%; Score 292; DB 6; Length 740;
Best Local Similarity 89.9%; Pred. No. 3.e-85;
Matches 313; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

61	ATCTCTGTCGTCGAGTAGAGTCTCTGTATAGGATGGCAAGACATACCTTGAATTGG	120	
141	ATCTCTGTCGTCGAGTAGAGTCTCTGTATAGGATGGCAAGACATACCTTGAATTGG	200	
121	TACCTGCAGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCA	180	
201	TACCTGCAGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATCAGATGTCCAACCTTGCC	260	
181	TCAGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC	240	
261	TCAGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC	320	
241	AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA	300	
321	AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCTCAAAATCTAGAGATTCTCT	380	
301	TTACAGTTCGGCCAAAGGACCAAGTGGAGATCAAAACGTACGGTGGCT	348	
381	CGGAGTTCGGCCAAAGGACCAAGTGGAGATCAAAACGTACGGTGGCT	428	
RESULT 4			
AX076855/c	AX076855	740 bp	
LOCUS	Sequence 3 from Patent WO0107082.	DNA	
DEFINITION	Sequence 3 from Patent WO0107082.	linear	
ACCESSION	AX076855	PAT 22-FEB-2001	
VERSION	AX076855.1		
KEYWORDS	GI:13121526		
SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		
REFERENCE	artificial sequences.		
AUTHORS	1 (bases 1 to 740)		
TITLE	Knick,V.C., Stimmel,J.B. and Thurmond,L.M.		
JOURNAL	Combination of an anti-ep-cam antibody with a chemotherapeutic agent		
FEATURES	Patent: WO 0107082-A 3 01-FEB-2001;		
source	GLAXO GROUP LIMITED (GB)		
	Location/Qualifiers		
	1..740		
	/organism="synthetic construct"		
	/db_xref="taxon:32630"		
	/note="Synthetic sequence"		
BASE COUNT	165 a 187 c 201 g 187 t		
ORIGIN			
Query Match	83.9%;	Score 292; DB 6; Length 740;	
Best Local Similarity	89.9%;	Pred. No. 3.3e-85;	
Matches 313; Conservative	0; Mismatches 35; Indels	0; Gaps	
QY	1	GATATTGTGATGACTCAGTCTCCACTCTCCTGCGCGTCAACCCCTGGAGAGCGGCTCC	60
Db	660	GATATTGTGATGACTCAGTCTCCACTCTCCTGCGCGTCAACCCCTGGAGAGCGGCTCC	601
QY	61	ATCTCTGTCGTCGAGTAGAGTCTCTGTATAGGATGGCAAGACATACCTTGAATTGG	120
Db	600	ATCTCTGTCGTCGAGTAGAGTCTCTGTATAGGATGGCAAGACATACCTTGAATTGG	541
QY	121	TACCTGCAGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCA	180
Db	540	TACCTGCAGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATCAGATGTCCAACCTTGCC	481
QY	181	TCAGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC	240
Db	480	TCAGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC	421
QY	241	AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA	300
Db	420	AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCTCAAAATCTAGAGATTCTCT	361
QY	301	TTACAGTTCGGCCAAAGGACCAAGTGGAGATCAAAACGTACGGTGGCT	348
Db	360	CGGAGTTCGGCCAAAGGACCAAGTGGAGATCAAAACGTACGGTGGCT	313

RESULT 5	
HSIGKL46	H.sapiens mRNA for rearranged Ig kappa light chain variable region (II.46).
LOCUS	410 bp mrna linear PRI 31-JAN-1994
DEFINITION	
ACCESSION	X72467.1 GI:441402
VERSION	
KEYWORDS	C-region; immunoglobulin; J-segment; kappa light chain; V-region.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Zachau,H.G.
TITLE	Direct Submission
JOURNAL	Submitted (26-APR-1993) H.G. Zachau, Institut fuer Physiologische Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen 2, FRG
REFERENCE	2 (bases 1 to 410)
AUTHORS	Klein,R., Jaenichen,R. and Zachau,H.G.
TITLE	Expressed human immunoglobulin kappa genes and their hypermutation
JOURNAL	Eur. J. Immunol. 23 (12), 3248-3262 (1993)
MEDLINE	94080891
PUBMED	8258341
FEATURES	Location/Qualifiers
source	1..410
	/organism="Homo sapiens"
	/isolate="M.I."
	/db_xref="taxon:9606"
	/chromosome="2"
	/clone="II.46"
	/tissue_type="spleen"
	/clone_lib="lambda zap II phage library"
	1..410
	/partial
	/codon_start=1
	/product="Ig kappa light chain (VJC)"
	/protein_id="CAA51135.1"
	/db_xref="GI:441403"
	/translation="MRLPAGLLGLMLWVGSGSDIVMTQSPPLSLPVTGPESASISCRSSQLRLSHSNYNLDYLRKPGSPQLLIYLGSNRASGYPDRESGSGSTDFTLKISRVEAEDGVGYCMQALQTPWTFGTGRKEIKRTVA"
V_region	1..410
	/product="Ig kappa light chain (VJC)"
V_segment	61..360
J_segment	361..399
	/note="J-kappa 1"
C_region	400..410
BASE COUNT	87 a 108 c 115 g 100 t
ORIGIN	
Query Match	79.8%; Score 277.6; DB 9; Length 410;
Best Local Similarity	87.4%; Pred. No. 1.8e-80;
Matches 304; Conservative	0; Mismatches 44; Indels 0; Gaps 0;
QY 1	GATATTGTGATGACTCTCCACTCTCCTGCCCGTCACCCCTGGAGAGCCGCCTCC 60
Db 61	GATATTGTGATGACTCTCCACTCTCCTGCCCGTCACCCCTGGAGAGCCGCCTCC 120
QY 61	ATCTCTCTGCGTCGAGTAAGAGTCTCTGTATAAGGATGGGAACATACTTTGAATTGG 120
Db 121	ATCTCTCTGAGGTCCTAGTCAGAGCCTCTCGCATAGTAATGGATACAACATTTGGATTGG 180
QY 121	TACCTCGAGAAGCCAGGGCAGTCTCCACAGTCTTGATCTATTGTGATCTCCACC CGGGCA 180
Db 181	TACCTCGAGAAGCCAGGGCAGTCTCCACAGTCTTGATCTATTGGTGTCTAATCGGGCCC 240
QY 181	TCAGGGGTCCTTCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 240
Db 241	TCGGGGGTCCTTCACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAAATC 300
QY 241	AGCAGAGTAGGAGGCTGAGGATGTTGGGTTTTATTACTGTCAACAGCTGGTAGATATCCA 300

```

Db 301 AGCAGAGTGGAGCTCAGGATGTTGGGGTTTATTACTGCAAGCTCTACAAACTCGG 360
      |||||
QY 301 TTCAGCTTGGCGCAAGGACCAAGGTGAGATCAAAAGTACGTTGGCT 348
      |||||
Db 361 TGGACGTTGGCGCAAGGACCAAGGTGGAATCAACAACTGTGGCT 408
      |||||

RESULT 6
HSA272080          353 bp mRNA linear PRI 16-NOV-2001
LOCUS              Homo sapiens partial mRNA for Immunoglobulin light chain variable
DEFINITION         region -Anti-F(ab')2 autoantibody (IGVL gene), isolate SN3.
ACCESSION          AJ272080
VERSION            AJ272080.1 GI:7024356
KEYWORDS            anti-F(ab')2; autoantibody; IGVL gene; immunoglobulin; light chain;
SOURCE              human.
ORGANISM            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS            Elagib,K.E., Borretzen,M., Vatn,I., Natvig,J.B. and Thompson,K.M.
TITLE              Characterization and V(H) sequences of human monoclonal
                   anti-F(ab')2 autoantibodies from normals and Sjogren's syndrome
                   patients
JOURNAL             Clin. Immunol. 98 (1), 62-69 (2001)
MEDLINE            20581359
PUBMED             11141328
REFERENCE
AUTHORS            Elagib,K.E.
TITLE              Direct Submission
JOURNAL             Submitted (21-FEB-2000) Elagib K.E., Laboratory for Rheumatology
                   Research, Institute of Immunology, Fr. Qvamsgate 1, N-172 Oslo,
                   NORWAY
FEATURES
Source              Location/Qualifiers
                     1..353
                     /organism="Homo sapiens"
                     /isolate="SN3"
                     /db_xref="taxon:9606"
                     /germline
                     1..353
                     /gene="IGVL"
                     <1..>353
                     /gene="IGVL"
                     /function="Anti-F(ab')2 autoantibody"
                     /codon_start=1
                     /evidence=experimental
                     /product="immunoglobulin light chain variable region"
                     /protein_id="CAB75876.1"
                     /db_xref="GI:7024357"
                     /db_xref="REMTREMBL:CAB75876"
                     /translation="DIVMTQSPLESLPVTPGEPAISCSRSSQSLHNSGYNVLDHWLQK
PGQSPQLILIGSNRAGSGVDFRFGSGSGDTFLKLSRVEADVGVIYTCMALQTPRT
FGQGTKEIRKTVAAAP"
BASE COUNT          81 a 94 c 93 g 85 t
ORIGIN
Query Match         79.3%; Score 276; DB 9; Length 353;
Best Local Similarity 87.1%; Pred. No. 6.le-80;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTCACCCCTGGAGAGCGGCGCTCC 60
      |||||
Db 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTCACCCCTGGAGAGCGGCGCTCC 60
      |||||
QY 61 ATCTCTCTGCTCGCTCGAGTAAGAGTCTCTCTGTATTAAGATGGGAAGACATCTATTGATTCG 120
      |||||
Db 61 ATCTCTCTGAGTCTAGTCACAGCGCTCTCTGCATAGTAAATGATACACTATTGTGATTCG 120
      |||||
QY 121 TACCTGCAGAACCCAGGCGACTCTCCACAGCTGCTGATCTATTGATGTCACCCCGGCA 180
      |||||
Db 121 TACCTGCAGAACCCAGGCGACTCTCCACAGCTGCTGATCTATTGATGTCATATTTGGTCTTAATCGGCGC 180
      |||||

```

```

QY 181 TCAGGGGTCCCTCAGAGGTTTCAGTGGCAGTCAGGCAGACAGATTTTACACTGAAATC 240
      |||||
Db 181 TCAGGGGTCCCTCAGAGGTTTCAGTGGCAGTCAGGCAGACAGATTTTACACTGAAATC 240
      |||||
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTCTCAACAGCTGGTAGAGTATFCCA 300
      |||||
Db 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTCTCAACAGCTGGTAGAGTATFCCA 300
      |||||
QY 301 TTCAAGCTTCGGCCCAAGGACCAAGGTGGAGTCAAAAGCTACGGTGGCT 348
      |||||
Db 301 CGTACGTTGGCCCAAGGACCAAGGTGGAATCAACGAAGTGTGGCT 348
      |||||

RESULT 7
HSTOP003          360 bp mRNA linear PRI 25-NOV-1998
LOCUS              H. sapiens mRNA for kappa immunoglobulin light chain (V-J-C region;
DEFINITION         clone HSTOP003).
ACCESSION          X93771
VERSION            X93771.1 GI:3928404
KEYWORDS            constant region; immunoglobulin; immunoglobulin kappa chain;
                   immunoglobulin light chain; joining region; variable region.
SOURCE              Homo sapiens
ORGANISM            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS            1 (bases 1 to 360)
                   Barington,T.
TITLE              Direct Submission
JOURNAL             Submitted (01-DEC-1995) Torben Barrington, Tissue Typing Laboratory
                   7631, Rigshospitalet, National University Hospital, Tagensvej 20,
                   DK-2200 Copenhagen N, DENMARK
REFERENCE
AUTHORS            2 (bases 1 to 360)
                   Barington,T., Hougs,L., Juul,L., Madsen,H.O., Ryder,L.P.,
                   Heilmann,C. and Svejgaard,A.
TITLE              The progeny of a single virgin B cell predominates the human recall
                   B cell response to the capsular polysaccharide of Haemophilus
                   influenzae type b
JOURNAL             J. Immunol. 157 (9), 4016-4027 (1996)
MEDLINE            97047794
PUBMED             8892635
COMMENT             On Nov 26, 1998 this sequence version replaced gi:1296757.
FEATURES
Source              Location/Qualifiers
                     1..360
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="2"
                     /clone="TOP003"
                     /cell_type="B lymphocyte"
                     /tissue_type="peripheral blood"
                     /rearranged
                     1..339
                     /gene="V-kappa-A3/A19 and J-kappa-3"
                     <1..339
                     /gene="V-kappa-A3/A19 and J-kappa-3"
                     /product="immunoglobulin kappa light chain"
                     /note="variable region and joining region"
                     340..>360
                     /note="constant region"
BASE COUNT          81 a 96 c 92 g 91 t
ORIGIN
Query Match         79.3%; Score 276; DB 9; Length 360;
Best Local Similarity 87.1%; Pred. No. 6.le-80;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTCACCCCTGGAGAGCGGCGCTCC 60
      |||||
Db 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTCACCCCTGGAGAGCGGCGCTCC 60
      |||||
QY 61 ATCTCTCTGCTCGCTCGAGTAAGAGTCTCTCTGTATTAAGATGGGAAGACATCTTGAATTCG 120
      |||||

```


[illegible]

```

MEDLINE 94080891
PUBMED 8258341
FEATURES
Source
Location/Qualifiers
1..407
/organism="Homo sapiens"
/isoate="M.B."
/db_xref="taxon:9606"
/chromosome="2"
/clone="II.8"
/tissue_type="spleen"
/clone_lib="lambda zap II phage library"
1..407
/partial
/notes="Protein sequence is in conflict with the conceptual translation"
/codon_start=3
/product="Ig kappa light chain (VJC)"
/protein_id="CAA51120.1"
/db_xref="GI:3980119"
/translation="MGLMLVYSGSDIVMTQSLPLVTPGEPASISCRSSQSLH NYLDWYLOKPGQSPOLLYLGSNRASGVPDRFSGSGGTDFTLKISRVEADVGVVYMOALQTPRTFGQGTKEIKRTVAAPCLS"
1..407
V_region
/product="Ig kappa light chain (VJC)"
V_segment
J_segment
342..380
/notes="J-Kappa 1"
C_region
87 a 107 c 110 g 103 t
BASE COUNT
ORIGIN
Query Match 79.3%; Score 276; DB 9; Length 377;
Best Local Similarity 87.1%; Pred. No. 6.1e-80;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60
Db 30 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 89
QY 61 ATCTCTGCTGCTCGAGTTCCTGTAAGGATGGGAGACATCTTGAATTGG 120
Db 90 ATCTCTGCTGCTCGAGTTCCTGTAAGGATGGGAGACATCTTGAATTGG 149
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGATGTCACCGCGGCA 180
Db 150 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGATGTCACCGCGGCA 209
QY 181 TCAGGGTCCCTGACAGTTCAGTGGGAGTGGATCAGGACAGATTTTACACTGAAATC 240
Db 210 TCAGGGTCCCTGACAGTTCAGTGGGAGTGGATCAGGACAGATTTTACACTGAAATC 269
QY 241 AGCAGAGTGGAGCTGAGGATCTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 270 AGCAGAGTGGAGCTGAGGATCTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 329
QY 301 TTCACCTTCGGCCCAAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348
Db 330 CTCACCTTCGGCCCAAGGACCAAGTGGAGATCAACAGTACGGTGGCT 377
RESULT 14
HSIGKLW31 407 bp mRNA linear PRI 04-DEC-1998
LOCUS H.sapiens mRNA for rearranged Ig kappa light chain variable region (II.8).
DEFINITION
ACCESSION X72452
VERSION X72452
KEYWORDS C-region; immunoglobulin; J-segment; kappa light chain; V-region.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 407)
Zachau, H.G.
Direct Submission
Submitted (26-APR-1993) H.G. Zachau, Institut fuer Physiologische Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen 2, FRG
2 (bases 1 to 407)
Klein, R., Jaenichen, R. and Zachau, H.G.
Expressed human immunoglobulin kappa genes and their hypermutation
JOURNAL, Eur. J. Immunol. 23 (12), 3248-3262 (1993)
MEDLINE 94080891
PUBMED 8258341
FEATURES
Source
Location/Qualifiers
1..407
/organism="Homo sapiens"
/isoate="M.B."
/db_xref="taxon:9606"
/chromosome="2"
/clone="II.8"
/tissue_type="spleen"
/clone_lib="lambda zap II phage library"
1..407
/partial
/notes="Protein sequence is in conflict with the conceptual translation"
/codon_start=3
/product="Ig kappa light chain (VJC)"
/protein_id="CAA51120.1"
/db_xref="GI:3980119"
/translation="MGLMLVYSGSDIVMTQSLPLVTPGEPASISCRSSQSLH NYLDWYLOKPGQSPOLLYLGSNRASGVPDRFSGSGGTDFTLKISRVEADVGVVYMOALQTPRTFGQGTKEIKRTVAAPCLS"
1..407
V_region
/product="Ig kappa light chain (VJC)"
V_segment
J_segment
342..380
/notes="J-Kappa 1"
C_region
87 a 107 c 110 g 103 t
BASE COUNT
ORIGIN
Query Match 79.3%; Score 276; DB 9; Length 377;
Best Local Similarity 87.1%; Pred. No. 6.1e-80;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 60
Db 30 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCACCCCTGGAGAGCGGCTCC 89
QY 61 ATCTCTGCTGCTCGAGTTCCTGTAAGGATGGGAGACATCTTGAATTGG 120
Db 90 ATCTCTGCTGCTCGAGTTCCTGTAAGGATGGGAGACATCTTGAATTGG 149
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGATGTCACCGCGGCA 180
Db 150 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTGATCTATTGATGTCACCGCGGCA 209
QY 181 TCAGGGTCCCTGACAGTTCAGTGGGAGTGGATCAGGACAGATTTTACACTGAAATC 240
Db 210 TCAGGGTCCCTGACAGTTCAGTGGGAGTGGATCAGGACAGATTTTACACTGAAATC 269
QY 241 AGCAGAGTGGAGCTGAGGATCTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 270 AGCAGAGTGGAGCTGAGGATCTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 329
QY 301 TTCACCTTCGGCCCAAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348
Db 330 CTCACCTTCGGCCCAAGGACCAAGTGGAGATCAACAGTACGGTGGCT 377
RESULT 15
HSTOP014 360 bp mRNA linear PRI 25-NOV-1998
LOCUS H.sapiens mRNA for kappa immunoglobulin light chain (V-J-C region; clone HSTOP014).
DEFINITION
ACCESSION X93772
VERSION X93772.1 GI:3928405
KEYWORDS constant region; immunoglobulin; immunoglobulin kappa chain; immunoglobulin light chain; joining region; variable region.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```


REFERENCE 1 (bases 1 to 360)
AUTHORS Barington,T.
TITLE Direct Submission
JOURNAL Submitted (01-DEC-1995) Torben Barington, Tissue Typing Laboratory
7631, Rigshospitalet, National University Hospital, Tagensvej 20,
DK-2200 Copenhagen N, DENMARK
REFERENCE 2 (bases 1 to 360)
AUTHORS Barington,T., Hougs,L., Juul,L., Madsen,H.O., Ryder,L.P.,
Heilmann,C. and Svejgaard,A.
TITLE The progeny of a single virgin B cell predominates the human recall
B cell response to the capsular polysaccharide of Haemophilus
influenzae type b
JOURNAL J. Immunol. 157 (9), 4016-4027 (1996)
MEDLINE 97047794
PUBMED 8892635
COMMENT On Nov 26, 1998 this sequence version replaced gi:1296758.
FEATURES
Location/Qualifiers
1..360
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="TOP014"
/cell_type="B lymphocyte"
/tissue_type="peripheral blood"
/rearranged
1..339
/gene="V-kappa-A3/A19 and J-kappa-3"
V_region <1..339
/gene="V-kappa-A3/A19 and J-kappa-3"
/product="immunoglobulin kappa light chain"
/note="variable region and joining region"
340..>360
C_region /note="constant region"
BASE COUNT 81 a 102 c 89 g 88 t
ORIGIN

Query Match 78.98; Score 274.4; DB 9; Length 360;
Best Local Similarity 86.88; Pred. No. 2.le-79;
Matches 302; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCCACCGCTGAGAGCGCGCTCC 60
|||||
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCCACCGCTGAGAGCGCGCTCC 60
QY 61 ATCTCTCTCGCTCGAGTAGAGTCTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
|||||
DB 61 ATCTCTCGAGTCTAGTCAGAGCTCTCTCATAGTAATGGCAACATCTATTTCGATTGG 120
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTATGTCACCGCGGCA 180
|||||
DB 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTGTTCCAAACGGCCC 180
QY 181 TCAGGGGTCCCTGCAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
|||||
DB 181 TCCGGGGTCCCTGCAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
QY 241 AGCAGAGTGGAGGCTGAGAGTTTGGGGTTTATTACTGTCAACAGCTGGTATAGTATCCA 300
|||||
DB 241 AGCAGAGTGGAGGCTGAGAGTTTGGGGTTTATTACTGTCAACAGCTGGTATAGTATCCA 300
QY 301 TTCAGGTTGGGCCAAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 348
|||||
DB 301 TTCAGTTCGGCCCTGGGACCAAGTGGATATCAAAAGTACGGTGGCT 348

Search completed: April 26, 2003, 06:31:05
Job time : 696.74 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:55:21 ; Search time 460.431 Seconds
(without alignments)
12240.775 Million cell updates/sec

Title: US-09-674-716b-17

Perfect score: 348
Sequence: 1 gatattgtgatcactcagtc.....agatcaaacgtacgtggct 348

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *

1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_estl: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: gb_gss: *
18: em_gss_hum: *
19: em_gss_inv: *
20: em_gss_pln: *
21: em_gss_vrt: *
22: em_gss_fun: *
23: em_gss_mam: *
24: em_gss_mus: *
25: em_gss_other: *
26: em_gss_pro: *
27: em_gss_rod: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	277.6	79.8	990	13	BI838327	BI838327	603083265
2	272.8	78.4	454	10	AW406883	AW406883	UI-HF-BLO
3	272.8	78.4	995	14	BQ712430	BQ712430	AGENCOURT
4	271.2	77.9	522	13	BM511309	BM511309	ij46b08.y
5	269.6	77.5	751	12	BG542438	BG542438	602569513
6	268.2	77.1	363	9	AA464313	AA464313	zx78c12.r

7	268	77.0	442	9	AA405415	AA405415	zu56d02.r
8	268	77.0	488	10	AW405725	AW405725	UI-HF-BLO
9	268	77.0	634	14	BM783161	BM783161	K-EST0061
10	267	76.7	491	12	BF174573	BF174573	MYE3409a
11	266.4	76.6	456	10	AW404683	AW404683	UI-HF-BLO
12	265	76.1	425	9	AI734035	AI734035	zu56d02.y
13	264.8	76.1	880	12	BG755003	BG755003	602711509
14	264.8	76.1	880	12	BG757588	BG757588	602714763
15	264.8	76.1	926	12	BG342051	BG342051	602463190
16	263.2	75.6	787	12	BG536224	BG536224	602565445
17	261.8	75.2	770	12	BG530186	BG530186	602558684
18	260	74.7	643	14	BM620052	BM620052	K-EST0088
19	259.6	74.6	410	12	BG059215	BG059215	nah51907.
20	259	74.4	468	12	BE829853	BE829853	RCG-ET007
21	259	74.4	908	12	BG685179	BG685179	602637065
22	256.8	73.8	462	12	BF176195	BF176195	MYE6594a
23	256	73.6	427	12	BF174767	BF174767	MYE3784.M
24	256	73.6	485	12	BF174421	BF174421	MYE3134a
25	255	73.3	958	14	BQ709417	BQ709417	AGENCOURT
26	254.4	73.1	730	13	BI837183	BI837183	603089959
27	254	73.0	474	12	BF175068	BF175068	MYE4339.M
28	253.6	72.9	952	12	BG758592	BG758592	602712820
29	252	72.4	597	12	BF868788	BF868788	IL3-ET011
30	252	72.4	650	13	BI765629	BI765629	603043768
31	252	72.4	898	14	BQ708918	BQ708918	AGENCOURT
32	252	72.4	960	14	BQ711007	BQ711007	AGENCOURT
33	251.2	72.2	859	12	BG758795	BG758795	602713155
34	250.8	72.1	488	14	H25625	H25625	Y448905.F1
35	248.8	71.5	492	12	BF870113	BF870113	IL3-ET011
36	248	71.3	424	12	BF176198	BF176198	MYE6598a
37	248	71.3	753	12	BG756401	BG756401	602715727
38	247.2	71.0	471	10	AW405772	AW405772	UI-HF-BLO
39	247.2	71.0	614	10	AW405187	AW405187	UI-HF-BLO
40	245.8	70.6	1220	14	BQ708355	BQ708355	AGENCOURT
41	245	70.4	931	12	BG757255	BG757255	602715238
42	241.8	69.5	475	12	BF174510	BF174510	MYE5291a
43	241.2	69.3	824	13	BI824708	BI824708	603033871
44	239.2	68.7	696	13	BI838136	BI838136	603083638
45	239.2	68.7	701	12	BG547597	BG547597	602575437

ALIGNMENTS

RESULT 1
BI838327
LOCUS 603083265F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:522297 5',
DEFINITION mRNA sequence.
ACCESSION BI838327
VERSION BI838327.1 GI:15949877
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 990)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11559 row: a column: 18
High quality sequence stop: 740.
Location/Qualifiers
1..990

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:522297"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
/Note="Organ: pooled pancreas and spleen; Vector:
pcmv-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: This is a NIH_MGC Library."
BASE COUNT      234 a 291 c 241 g 224 t
ORIGIN
Query Match      79.8%; Score 277.6; DB 13; Length 990;
Best Local Similarity 87.4%; Pred. No. 7.9e-73;
Matches 304; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTACCCCTGGAGAGCGGCGCTCC 60
Db 87 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTACCCCTGGAGAGCGGCGCTCC 146
Qy 61 ATCTCTCTGTCGCTCGAGTAAAGAGTCTCCTGTATTAAGGATGGGAAGACATACCTTGAATTGG 120
Db 147 ATCTCTCTGAGTCTAGTCAGAGGCTCCTGTCATATAACGGATACAAGTATTGTTGATTGG 206
Qy 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGTATTTGATGTCACCCCGGGCA 180
Db 207 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGTATTTGATGTCACCCCGGGCC 266
Qy 181 TCAGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACACAGATTTTACACTGAAATC 240
Db 267 TCCGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACACAGATTTTACACTGAAATC 326
Qy 241 AGCAGAGTGAGGCTCAGGATGTTGGGTTTATTACTGCAACAGCTGGTAGAGTATCCA 300
Db 327 AGCAGAGTGAGGCTCAGGATGTTGGGTTTATTACTGCGTGAGTCTCTACAAACCCCG 386
Qy 301 TTCACGTTCCGCCAAGGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
Db 387 CTCACTTTCGGCGGAGGAGCAAGGTGGAGATCAAAACGTACGGTGGCT 434

RESULT 2
AW406883
LOCUS      UI-HF-BL0-adg-h-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
DEFINITION IMAGE:3061493 5', mRNA sequence.
ACCESSION AW406883
VERSION    EST.
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 454)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgabbs@mail.nih.gov
           Eco RI site shown at the beginning of the sequence.
           Tissue procurement: Louis M. Staudt, M.D., Ph.D.
           cDNA Library Preparation: M.B. Soares Lab
           cDNA Library Arrayed by: M.B. Soares Lab
           DNA Sequencing by: M.B. Soares Lab
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           www.bio.llnl.gov/dbrrp/image/image.html
           Seq primer: M13 Forward.

```

```

FEATURES             Location/Qualifiers
     source            1..454
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3061493"
                     /clone_lib="NIH_MGC_37"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /Note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT      104 a 122 c 114 g 114 t
ORIGIN
Query Match      78.4%; Score 272.8; DB 10; Length 454;
Best Local Similarity 86.5%; Pred. No. 1.5e-71;
Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTACCCCTGGAGAGCGGCGCTCC 60
Db 16 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTACCCCTGGAGAGCGGCGCTCC 75
Qy 61 ATCTCTCTGTCGCTCGAGTAAAGAGTCTCCTGTATTAAGGATGGGAAGACATACCTTGAATTGG 120
Db 76 ATCTCTCTGAGTCTAGTCAGAGGCTCCTGTCATATAAGGATACAAGTATTGTTGATTGG 135
Qy 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGTATTTGATGTCACCCCGGGCA 180
Db 136 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGTATTTGATGTCACCCCGGGCC 195
Qy 181 TCAGGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACACAGATTTTACACTGAAATC 240
Db 196 TCCGGGTCCCTGCACAGGTTTCAGTGGCAGTGGATCAGGCACACAGATTTTACACTGAAATC 255
Qy 241 AGCAGAGTGAGGCTCAGGATGTTGGGTTTATTACTGCAACAGCTGGTAGAGTATCCA 300
Db 256 AACAAAGTGGAGGCTCAGGATGTTGGGTTTATTACTGCAATGCAAGCTCTACAAACCTCT 315
Qy 301 TTCACGTTCCGCCAAGGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
Db 316 CAGACGTTCCGCCAAGGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 363

RESULT 3
BQ712430
LOCUS      BQ712430
DEFINITION AGENCOURT_8352203 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277729
           5', mRNA sequence.
ACCESSION BQ712430
VERSION    BQ712430.1 GI:21851329
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 995)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgabbs@mail.nih.gov
           Tissue Procurement: Dr. Mark Watson
           cDNA Library Preparation: Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Agencourt Bioscience Corporation
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCW2464 row: j column: 02

```


approx. 1x10⁶. Clones from the primary library were randomly selected for single pass sequencing."

BASE COUNT 102 a 136 c 128 g 124 t 1 others
ORIGIN

Query Match 76.7%; Score 267; DB 12; Length 491;
Best Local Similarity 85.3%; Pred. No. 8.6e-70;
Matches 297; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTTCACCTCTCCCTGCGCTCCACCTCGGAGCGGCGCTCC 60
DB 81 GATATTGTGATGACTTCACCTCTCCCTGCGCTCCACCTCGGAGCGGCGCTCC 140
QY 61 ATCTCCTGCTGCGTTCAGTAAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATGG 120
DB 141 ATCTCCTGCTGCGTTCAGTAAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATGG 200
QY 121 TACCTGCAGAGCCAGGCGCTGCTCCACAGCTCTCTGATCTATTTGATGTCACCGCGGCA 180
DB 201 TACCTGCAGAGCCAGGCGCTGCTCCACAGCTCTCTGATCTATTTGATGTCACCGCGGCA 260
QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 261 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 320
QY 241 ACAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGTGGTAGAGTATCCA 300
DB 321 ACAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGTGGTAGAGTATCCA 380
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 348
DB 381 CAGACTTTTGGCCAGGGACCAAGTGGAGATCAAAAGTACGGTGGCT 428

RESULT 11
AW404683
LOCUS
DEFINITION
IMAGE:3058464 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW404683 456 bp mRNA linear EST 16-FEB-2000
UI-HF-BLO-acd-a-01-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
IMAGE:3058464 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
Location/Qualifiers

FEATURES
source

1..456
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3058464"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: p7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA

(1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 99 a 121 c 117 g 119 t
ORIGIN

Query Match 76.6%; Score 266.4; DB 10; Length 456;
Best Local Similarity 85.3%; Pred. No. 1.3e-69;
Matches 297; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTTCACCTCTCCCTGCGCTCCACCTCGGAGCGGCGCTCC 60
DB 21 GATATTGTGATGACTTCACCTCTCCCTGCGCTCCACCTCGGAGCGGCGCTCC 80
QY 61 ATCTCCTGCTGCGTTCAGTAAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATGG 120
DB 81 ATCTCCTGCTGCGTTCAGTAAGAGTCTCTGTATAAGGATGGGAAGACATACCTTGAATGG 140
QY 121 TACCTGCAGAGCCAGGCGCTGCTCCACAGCTCTCTGATCTATTTGATGTCACCGCGGCA 180
DB 141 TACCTGCAGAGCCAGGCGCTGCTCCACAGCTCTCTGATCTATTTGATGTCACCGCGGCA 200
QY 181 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 201 TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 260
QY 241 ACAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGTGGTAGAGTATCCA 300
DB 261 ACAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGTGGTAGAGTATCCA 320
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 348
DB 321 ATCAGTTCGGCCAGGACCAAGTGGAGATCAAAAGTACGGTGGCT 368

RESULT 12
AI734035
LOCUS
DEFINITION

AI734035 425 bp mRNA linear EST 24-OCT-2000
zu56d02.y5 Soares ovary tumor Nhot Homo sapiens cDNA clone
IMAGE:741987 5', similar to gb:X72467 IG KAPPA CHAIN PRECURSOR V-II
REGION (HUMAN);, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Other ESTs: zu56d02.s1
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: WashU-NCI human EST Project
This read has been verified (found to hit its original self in the
correct orientation)
Insert Length: 1053 Std Error: 0.00
Seq primer: -40RP from Gibco.
Location/Qualifiers

FEATURES
source

1..425
/organism="Homo sapiens"
/db_xref="GDB:5942254"
/db_xref="taxon:9606"
/clone="IMAGE:741987"
/clone_lib="Soares ovary tumor Nhot"
/sex="Female"
/tissue_type="ovarian tumor"


```

source
1. .880
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:485095"
/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DHI0B (phage-resistant)"
/site="Organ: B-cells; Vector: pOTB7; site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
BASE COUNT      201 a 225 c 223 g 200 t
ORIGIN
Query Match      76.1%; Score 264.8; DB 12; Length 880;
Best Local Similarity 85.1%; Pred. No. 5.4e-69;
Matches 296; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGGCTCC 60
DB 71 GAAATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGGCTCC 130
QY 61 ATCTCTCTGCTCGAGTAGAGTCTCTGTATTAAGATGGGAAGACATCTTGAATTGG 120
DB 131 ATCTCTCTGAGGTCTAGTCAGAGCTCTCTGCATAGCAATGGATACACCTATTGGATTGG 190
QY 121 TACCTGCAAGAGCCAGGCGAGTCTCCACAGCTCTGTATTTGATGTCCACCCGGGCA 180
DB 191 TACCTGCAAGAGCCGGGCGAGTCTCCACAACTCTGTATTTGGTCTTAATCGGGCC 250
QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCGGACACAGTTTACACTGAAATC 240
DB 251 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCGGACACAGTTTACACTGAAATC 310
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 311 AACAGATGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGTACAACTCC 370
QY 301 TTCAGTTCGGCCAAAGGACCAAGTGGAGATCAAACTGACGGTGGCT 348
DB 371 TTCACTTTCGGCCCTGGGACCAAGTGGAAATCAACAGCACTGTGGCT 418

RESULT 15
BG342051
LOCUS      BG342051          926 bp    mRNA    linear    EST 27-FEB-2001
DEFINITION 602463190F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:457518 5',
mRNA sequence.
ACCESSION  BG342051
VERSION    BG342051.1  GI:13148477
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 926)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
           cDNA Library Preparation: Ling Hong/Rubin Laboratory
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov

```

```

Plate: LLCMI287 row: d column: 23
High quality sequence stop: 558.
FEATURES             Location/Qualifiers
     source            1..926
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:457518"
                     /clone_lib="NIH_MGC_48"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DHI0B (phage-resistant)"
                     /notes="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      221 a 242 c 245 g 218 t
ORIGIN
Query Match      76.1%; Score 264.8; DB 12; Length 926;
Best Local Similarity 87.1%; Pred. No. 5.6e-69;
Matches 303; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGGCTCC 60
DB 81 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGGCTCC 140
QY 61 ATCTCTCTGCTCGAGTAAAGAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 120
DB 141 ATCTCTCGAGGTCTAGTCAGAGCTCTCTGTAT---GATGGATACAACTATTGGATTGG 197
QY 121 TACCTGCAAGAGCCAGGCGAGTCTCCACAGCTCTCTGTATTTGATGTCCACCCGGGCA 180
DB 198 TACTTTCAGAGACCCAGGCGAGTCTCCACAGCTCTCTGTATTTTGGTTCTAATCGGGCC 257
QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCGGACACAGATTTACACTGAAATC 240
DB 258 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCGGACACAGATTTACACTGAAATC 317
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 318 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGTACAAATCCG 377
QY 301 TTCAGTTCGGCCAAAGGACCAAGTGGAGATCAAACTGACGGTGGCT 348
DB 378 TGGAGCTTCGGCCAAAGGACCAAGTGCAAATCAACAGCACTGTGGCT 425

Search completed: April 26, 2003, 07:26:47
Job time : 464.431 secs

```


GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:50:01 ; Search time 70.0118 seconds
(without alignments)
11193.756 Million cell updates/sec

Title: US-09-674-716b-17

Perfect score: 348

Sequence: 1 gatattgtatgactcagtc.....agatcaaacgtacgttggtc 348

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	348	100.0	348	21	AAZ34747		Humanised anti-CD22
2	292	83.9	740	22	AAF63373		Humanised 323/A3 (
3	292	83.9	740	22	AAF63377		Anti-Ep-CAM antibo
4	276	79.3	772	20	AAZ24418		Human bladder tumo
5	274	78.7	720	21	AAAL3927		Human PTHrp monocl
6	273	78.4	720	21	AAAL3924		Human PTHrp monocl
7	272.8	78.4	720	21	AAAL3925		Human PTHrp monocl
8	272.4	78.3	720	21	AAAL3928		Human PTHrp monocl
9	271.8	78.1	720	21	AAAL3920		Human PTHrp monocl

10	270.8	77.8	720	21	AAAL3926	Human PTHrp monocl
11	269.6	77.5	720	21	AAAL3921	Human PTHrp monocl
12	268.2	77.1	720	21	AAAL3923	Human PTHrp monocl
13	267.8	77.0	720	21	AAAL3929	Human PTHrp monocl
14	266.6	76.6	720	21	AAAL3922	Human PTHrp monocl
15	263.2	75.6	963	22	AAF44895	Human breast cance
16	263	75.6	1143	22	AAAD20732	Human bivPHI-IL-2
17	262.8	75.5	339	22	AAAD20730	Human PHL Fab anti
18	262.8	75.5	663	22	AAAD20744	Human recombinant
19	261.2	75.1	339	15	AAQ70940	Anti-CMV monoclon
20	258.8	74.4	342	21	AAAZ27664	DNA encoding anti-
21	258.4	74.3	417	22	AAH41159	Human coding seque
22	257.2	73.9	437	21	AAZ34746	Mouse anti-CD23 MA
23	257.2	73.9	744	22	AAH47762	Anti-hEDRF antibod
24	253.4	72.8	651	20	AAZ24421	Human bladder tumo
25	252.8	72.6	336	19	AAV10325	Human Mab AB17.1.4
26	252	72.4	336	22	AAH68644	Human anti-Rh(D) c
27	251.6	72.3	336	21	AAAG6160	Nucleotide sequenc
28	250.4	72.0	444	20	AAZ20410	Igm antibody CEM 1
29	249.4	71.7	339	17	AAAT10942	Vlkappa coding seq
30	245.6	70.6	381	24	ABK48973	DNA encoding light
31	245.6	70.6	720	19	AAV61359	Anti-human Fas hum
32	245.6	70.6	720	21	AAV78267	Anti-human Fas imm
33	244	70.1	420	19	AAV03802	DNA encoding the l
34	244	70.1	464	14	AAQ33097	C242:11 Mab kappa
35	244	70.1	464	14	AAQ36950	C242 kappa chain v
36	244	70.1	720	19	AAV61360	Anti-human Fas hum
37	244	70.1	720	19	AAV61361	Anti-human Fas hum
38	244	70.1	720	21	AAV78268	Anti-human Fas imm
39	244	70.1	720	21	AAV78269	Anti-human Fas imm
40	243.6	70.0	340	19	AAV09791	DNA encoding the l
41	242.4	69.7	720	19	AAV61362	Anti-human Fas hum
42	242.4	69.7	720	21	AAV78270	Anti-human Fas imm
43	242	69.5	793	24	ABK43188	DNA encoding const
44	242	69.5	1111	24	ABK43191	DNA encoding fiber
45	242	69.5	1402	24	ABK43192	DNA encoding fiber

ALIGNMENTS

RESULT 1
AAZ34747
ID AAZ34747 standard; cDNA; 348 BP.
XX AC
XX AAZ34747;
XX
DT 15-FEB-2000 (first entry)
XX
DE Humanised anti-CD23 Mab C11 light chain variable region cDNA.
XX
KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes;
KW B-cell malignancy; therapy; ds.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO9958679-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-GB01434.
XX
XX 09-MAY-1998; 98GB-0009839.
XX


```
|||||
Db 381 CGGACGTTCCGCGCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 428
|||||
RESULT 3
AAF63377/c
ID AAF63377 standard; DNA; 740 BP.
XX
AC AAF63377;
XX
DT 10-MAY-2001 (first entry)
XX
DE Anti-Ep-CAM antibody related DNA sequence SEQ ID 3.
XX
KW Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;
KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer; ds.
XX
OS Unidentified.
XX
PN WO200107082-A1.
XX
PD 01-FEB-2001.
XX
PF 23-JUL-1999; 99WO-EP05271.
XX
PR 23-JUL-1999; 99WO-EP05271.
XX
PA (GLAX ) GLAXO GROUP LTD.
XX
PI Knick VC, Stimmel JB, Thurmond LM;
XX
DR WPI; 2001-182729/18.
XX
PT Combination for treating cancer (e.g. breast, gastric or prostate
PT cancers), or in the manufacture of a medicament for anti-cancer
PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody
PT with a chemotherapeutic agent -
XX
PS Disclosure; Page 66; 103pp; English.
XX
CC This invention relates to a combination of an anti-Ep-CAM (cyclic
CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is
CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)
CC phase or the second growth phase (M) of cell enlargement (G2)/DNA
CC replication. The antibody exhibits cytostatic activity and is useful in
CC the manufacture of a medicament for use in anti-cancer therapy.
CC characterised in that a chemotherapeutic agent, which is capable of
CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is
CC co-administered to a patient with an anti-Ep-CAM antibody. The
CC combination is useful for treating cancer, particularly colorectal
CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell
CC lung cancer. The present sequence represents DNA related to the
CC anti-Ep-CAM antibody used in the combination of the invention.
XX
SQ Sequence 740 BP; 165 A; 187 C; 201 G; 187 T; 0 other;
Query Match 83.9%; Score 292; DB 22; Length 740;
Best Local Similarity 89.9%; Pred. No. 1.8e-80;
Matches 313; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCGCGCTCC 60
|||||
Db 660 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCGCGCTCC 601
QY 61 ATCTCCTGTCGCTCGAGTAAAGTCTCCTGTATAGGATGGGAACATCTTGAATTGG 120
|||||
Db 600 ATCTCCTGTAGTCTAGTAAAGATCTCCTGTCATGTAATGGCATCTTATTGTATTGG 541
QY 121 TACTCTCAGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGTATGTCCACCGCGCA 180
|||||
Db 540 TACTCTCAGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATCAGATGTCCAACTTGC 481
QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
|||||
Db 480 TCAGGGGTCCCTGACAGGTTTCAGTGGATCAGGCACAGATTTTACACTGAAATC 421
|||||
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
|||||
Db 420 AGCAGAGTGGAGGCTGAGGATTTGGGTTTATTACTGTCTCAAAATCTAGAGATTCTCT 361
|||||
QY 301 TTCACGTTCCGCCCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
|||||
Db 360 CGGACGTTCCGCCCAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 313
|||||
RESULT 4
AAZ24418
ID AAZ24418 standard; cDNA; 772 BP.
XX
AC AAZ24418;
XX
DT 14-FEB-2000 (first entry)
XX
DE Human bladder tumour cDNA library derived EST 30.
XX
KW Expressed sequence tag; human; bladder; tumour; cancer; cytostatic;
KW treatment; gene therapy; EST; ss.
XX
OS Homo sapiens.
XX
PN DE19818619-A1.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1998; 98DE-1018619.
XX
PR 21-APR-1998; 98DE-1018619.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
XX
DR WPI; 1999-612028/53.
XX
PT New nucleic acid sequences expressed in bladder tumor tissue, and
PT derived polypeptides, for treatment of bladder tumor and identification
PT of therapeutic agents -
XX
PS Claim 3; Page 84; 132pp; German.
XX
CC This invention describes novel polypeptide fragments (I) and the
CC polynucleotides (II) that encode them that are highly expressed in a
CC human bladder tumour and which have cytostatic activity. (II) are used
CC for recombinant expression of (I) and to isolate complete genes. (I) are
CC used to identify agents suitable for treatment of bladder cancer, to
CC directly treat this form of cancer (including expression from gene
CC therapy vectors) or are used in a preparation for cancer treatment. (I)
CC is also used for the generation of specific antibodies. (II) are
CC identified by assembling ESTs (expressed sequence tags) from a
CC particular tissue type before comparison of the gene to be revealed, and
CC allows a significantly longer fragment of the gene to be revealed, and
CC therefore reduces the number of failures associated with the fact that
CC ESTs from different libraries may represent different parts of the same
CC unknown gene, distorting the estimated frequency of occurrence in a
CC particular tissue. AAZ43260-243309 represent expressed sequence tag (EST)
CC fragments isolated from a human bladder tumour cDNA library which encode
CC the proteins represented in AAY66143-Y66198.
XX
SQ Sequence 772 BP; 181 A; 210 C; 206 G; 175 T; 0 other;
Query Match 79.3%; Score 276; DB 20; Length 772;
Best Local Similarity 87.1%; Pred. No. 1.7e-75;
Matches 303; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCGCGCTCC 60
|||||
```

```
Db 87 GATATTGTGACTAGTCTCCACTCTCCCTGCCCCCTACCCCTGGAGAGCGCGCTCC 146
QY 61 ATCTCTGTCTCGTAGTAAGAGTCTCTCTGTATAAGGATGGGAAGACATATCTTGAATTGG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 147 ATCTCTGTGAGGCTCTAGTCAGAGGCTCTCTGCATAGTAATGATGATCAACATATTTGGATTGG 206
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGATGCCACCGCGGCA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 207 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGATGCCACCGCGGCA 266
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TCAGGGTCCCTGCACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 267 TCCGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 326
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 327 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 386
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAACAGTACGGTGGCT 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 387 CTCACTTTCGGCGGAGGACCAAGGTGGAGATCAACAGTACGGTGGCT 434
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
AAAL13927
ID AAAL13927 standard; DNA; 720 BP.
XX
AC AAAL13927;
XX
XX 02-AUG-2000 (first entry)
DT
DE Human PTHrP monoclonal antibody clone 3G4-3 DNA SEQ ID NO:17.
XX
XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.
XX
XX Homo sapiens.
OS
XX JP2000080100-A.
PN
XX 21-MAR-2000.
PD
XX 12-OCT-1998; 98JP-0304793.
PF
XX 17-JUN-1998; 98JP-0188196.
PR
XX 26-JUN-1998; 98JP-0196729.
PR
XX (NISR ) JAPAN TOBACCO INC.
PA
XX WPI; 2000-286723/25.
-DR
XX P-PSDB; AAY82617.
XX
XX A human monoclonal antibody to parathyroid hormone related protein.
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain
XX
XX Example 10; Page 50; 88pp; Japanese.
PS
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a
XX human PTHrP monoclonal antibody clone nucleotide sequence from the
```

```
CC present invention.
XX
SQ Sequence 720 BP; 174 A; 191 C; 188 G; 163 T; 4 other;
XX
Query Match 78.7%; Score 274; DB 21; Length 720;
Best Local Similarity 86.5%; Pred. No. 7e-75;
Matches 301; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCAGTCTCCACTCTCCCTGCCCCCTACCCCTGGAGAGCGCGCTCC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GATATTGTGATGACTCAGTNTCCACTCTCCCTGCCCCCTACCCCTGGAGAGCGCGCTCC 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 ATCTCTGTCTCGTAGTAAGAGTCTCTCTGTATAAGGATGGGAAGACATATCTTGAATTGG 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 ATTTCTCTCAGGCTCTAGTCAGAGCTCTCTGATAGTAGTATGAAACAACTATTTGGATTGG 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCCACAGTCTCTGATCTATTTGATGCCACCGCGGCA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTTGATGCCACCGCGGCA 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 TCAGGGTCCCTGCACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 TCCGGGTCCCTGACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 301 TTCACGTTCCGCCAAGGACCAAGGTGGAGATCAACAGTACGGTGGCT 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 TTCACTTTCGGCGGAGGACCAAGGTGGAGATCAACAGTACGGTGGCT 408
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
AAAL13924
ID AAAL13924 standard; DNA; 720 BP.
XX
AC AAAL13924;
XX
XX 02-AUG-2000 (first entry)
DT
DE Human PTHrP monoclonal antibody clone 2F8-10-3 DNA SEQ ID NO:11.
XX
XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.
XX
XX Homo sapiens.
OS
XX JP2000080100-A.
PN
XX 21-MAR-2000.
PD
XX 12-OCT-1998; 98JP-0304793.
PF
XX 17-JUN-1998; 98JP-0188196.
PR
XX 26-JUN-1998; 98JP-0196729.
PR
XX (NISR ) JAPAN TOBACCO INC.
PA
XX WPI; 2000-286723/25.
-DR
XX P-PSDB; AAY82614.
XX
XX A human monoclonal antibody to parathyroid hormone related protein.
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain
XX
XX Example 10; Page 41-42; 88pp; Japanese.
PS
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
```


its fragments, following the stimulation of pPhrP has the following properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits the release of calcium from bone; or (c) inhibits elevation of blood calcium content. The monoclonal antibody can be used in the treatment of hypercalcaemia, rheumatoid arthritis, cancer of bone including metastasis, pain, fracture, cachexia, diseases of teeth, periodontal diseases and gingiva, sepsis, systemic inflammatory response syndrome (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and antiinflammatory activities. The present sequence represents a human pPhrP monoclonal antibody clone nucleotide sequence from the present invention.

[illegible]

RESULT	7
AAAI3925	
ID	AAAI3925 standard; DNA; 720 BP.
XX	
XX	
AC	AAAI3925;
XX	
DT	02-AUG-2000 (first entry)
XX	
XX	Human PTHRp monoclonal antibody clone 1C1-3 DNA SEQ ID NO:13.
DE	
XX	
KW	Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW	hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW	fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW	sepsis; systemic inflammatory response syndrome; SIRS;
KW	hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.

DR	P-PSDB; AAY82615.
XX	
PT	A human monoclonal antibody to parathyroid hormone related protein. -
PT	useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone
PT	including metastasis, and pain
XX	
XX	Example 10; Page 44-45; 88pp; Japanese.
XX	
CC	The present invention describes a human monoclonal antibody to
CC	parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC	its fragments, following the stimulation of PTHrP has the following
CC	properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC	the release of calcium from bone; or (c) inhibits elevation of blood
CC	calcium content. The monoclonal antibody can be used in the treatment
CC	of hypercalcemia, rheumatoid arthritis, cancer of bone including
CC	metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC	diseases and gingiva, sepsis, systemic inflammatory response syndrome
CC	(SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC	antiinflammatory activities. The present sequence represents a
CC	human PTHrP monoclonal antibody clone nucleotide sequence from the
CC	present invention.
XX	
XX	Sequence 720 BP; 172 A; 197 C; 190 G; 160 T; 1 other;
XX	

Query Match	78.4%	Score 272.8	DB 21	Length 720
Best Local Similarity	86.5%	Pred. No. 1.6e-74		
Matches 301	Conservative 0	Mismatches 47	Indels 0	Gaps 0
Qy	1	GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCGTACCCCTCGAGAGCCGCGCTCC	60	
Db	61	GATATTGTGATGACTCAGTCCCCACTTCCCTGCGCCGTACCCCTCGAGAGCCGCGCTCC	120	
Qy	61	ATCTCCTGTCTCGAGTAAGAGTCTCTGTATTAAGGATGGGAACATCTTGAATTGG	120	
Db	121	ATCTCCTGCAGGTCTAGTCAGAGCCTCTCTGATAGTAATGGGAATACTATTGGATTGG	180	
Qy	121	TACCTGCAAGAGCAGGGCAGTCTCCACAGCTCCTGATCTATTGTAGTGTCCACCCGGGCA	180	
Db	181	TACCTGCAGAAGCAGGGCAGTCTCCACAGCTCCTGATCTATTGGGTTCCTAATCGGGCC	240	
Qy	181	TCAGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC	240	
Db	241	TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC	300	
Qy	241	AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA	300	
Db	301	AGCAGGTGGAGGCTGAGGATGTTGGGGATTATTACTGCATGCAAGCTCTACAACTCCA	360	
Qy	301	TTTACGTTTCGCCAAGGGACCAAGGTGGAGATCAAAAGTACCGTGGCT	348	
Db	361	TTTACTTTTCGGCCCTGGGACCAAGTGGATATCAAAAGTATGGCT	408	

RESULT 8	
AAAL3928	
ID	AAAL3928 standard; DNA; 720 BP.
XX	
XX	
AC	AAAL3928;
XX	
DT	02-AUG-2000 (first entry)
XX	
XX	
DE	Human PTHrP monoclonal antibody clone 4B4-6-21 DNA SEQ ID NO:19.
XX	
KW	Human: parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW	hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW	fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW	sepsis; systemic inflammatory response syndrome; SIRS;
XX	hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.
XX	
OS	Homo sapiens.
XX	
PN	JP2000080100-A.
XX	

```

PD 21-MAR-2000.
XX
PF 12-OCT-1998; 98JP-0304793.
XX
PR 17-JUN-1998; 98JP-0188196.
XX
PR 26-JUN-1998; 98JP-0196729.
XX
PA (NISB ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-286723/25.
XX
XX P-PSDB; AAY82618.
XX
PT A human monoclonal antibody to parathyroid hormone related protein.
PT useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain
XX
XX Example 10; Page 53-54; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a
XX human PTHrP monoclonal antibody clone nucleotide sequence from the
XX present invention.
XX
XX Sequence 720 BP; 174 A; 191 C; 186 G; 162 T; 7 other;
XX
Query Match 78.3%; Score 272.4; DB 21; Length 720;
Best Local Similarity 86.2%; Pred. No. 2.2e-74;
Matches 300; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGGTCACCCCTGGAGAGCGGCTCC 60
DB 61 GATATTGTGATGANTCAGTNTCCACTCTCCCTGCGGTCACCCCTGGAGAGCGGCTCC 120
QY 61 ATCTCTCTGCTCGAGTAAAGAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 120
DB 121 ATCTCTCTGAGGCTAGTACAGGCTCTGAATAGTAAAGTACAACTATTTCGATTGG 180
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGTTGATGCCACCGGCA 180
DB 181 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGTTGGTCTTAATCGG 240
QY 181 TCAGGGTCTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAA 240
DB 241 TCCGGGTCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAA 300
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
DB 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 360
QY 301 TTCAGGTTTCGGCCAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
DB 361 TTCAGTTTCGGCCCTGGGACCAAGTGGATATCAACAGCAACTGTGGCT 408

```

RESULT 9

AAAL13920

ID AAAL13920 standard; DNA; 720 BP.

XX AC

XX AAAL13920;

XX 02-AUG-2000 (first entry)

XX DE

XX Human PTHrP monoclonal antibody clone 15H7-8-3 DNA SEQ ID NO:3.

XX

XX

```

RESULT 10
AAAI3926
ID   AAAI3926 standard; DNA; 720 BP.
XX
AC   AAAI3926;
XX
DT   02-AUG-2000 (first entry)
XX
DE   Human PTHrP monoclonal antibody clone 264-12-20 DNA SEQ ID NO:15.
XX
KW   Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW   hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW   fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW   sepsis; systemic inflammatory response syndrome; SIRS;
KW   hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds..
XX
OS   Homo sapiens.
XX
PN   JP2000080100-A.
XX
PD   21-MAR-2000.
XX
PF   12-OCT-1998; 98JP-0304793.
XX
PR   17-JUN-1998; 98JP-0188196.
XX
PR   26-JUN-1998; 98JP-0196729.
XX
PA   (NITSB ) JAPAN TOBACCO INC.
XX
WPI; 2000-286723/25.
XX
P-PSDB; AAY82616.
XX
PT   A human monoclonal antibody to parathyroid hormone related protein. -
PT   useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT   including metastasis, and pain
XX
PS   Example 10; Page 48-49; 88pp; Japanese.
XX
CC   The present invention describes a human monoclonal antibody to
CC   parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC   its fragments, following the stimulation of PTHrP has the following
CC   properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC   the release of calcium from bone; or (c) inhibits elevation of blood
CC   calcium content. The monoclonal antibody can be used in the treatment
CC   of hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC   metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC   diseases and gingiva, sepsis, systemic inflammatory response syndrome
CC   (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC   antiinflammatory activities. The present sequence represents a
CC   human PTHrP monoclonal antibody clone nucleotide sequence from the
CC   present invention.
XX
SQ   Sequence 720 BP; 172 A; 193 C; 187 G; 163 T; 5 other;

Query Match      77.8%; Score 270.8; DB 21; Length 720;
Best Local Similarity 85.9%; Pred. No. 6.8e-74;
Matches 299; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY   1 GATATTGTGATGACTCAGTCTCCACACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCCCTCC 60
DB   61 GATATTGTGATGANTCAGTNTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCCCTCC 120

QY   61 ATCTCTCTGCTCGCTAGAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 120
DB   121 ATCTCTCTCAGGTCTAGTCAGAGCCCTCTTCATAGTANTGGATACACTATTTGGATTGG 180

QY   121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGTATGTCACCCGGGCA 180
DB   181 TTCCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGTGGTTTCTAATCGGGCC 240

QY   181 TCAGGGGTCCCTGCAGAGTTTCAGTGGCGAGTGGATCAGGCACAGATTTTACCTGAAATC 240
DB   241 TCCGGGGTCCCTGCAGAGTTTCAGTGGCGAGTGGATCAGGCACAGATTTTACCTGAAATC 300

```

```

QY   241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB   301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTACAAACTCCA 360
XX
QY   301 TTCAGGTTTCGCCCAAGGACCAAGGTGGAGATCAAAACGTACCGTGGCT 348
DB   361 TTCACTTTCGCCCTGGGACCAAGTGGATATCAACAGCAACTGTGGCT 408

RESULT 11
AAAI3921
ID   AAAI3921 standard; DNA; 720 BP.
XX
AC   AAAI3921;
XX
DT   02-AUG-2000 (first entry)
XX
DE   Human PTHrP monoclonal antibody clone 16E12-6 DNA SEQ ID NO:5.
XX
KW   Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW   hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW   fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW   sepsis; systemic inflammatory response syndrome; SIRS;
KW   hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds..
XX
OS   Homo sapiens.
XX
PN   JP2000080100-A.
XX
PD   21-MAR-2000.
XX
PF   12-OCT-1998; 98JP-0304793.
XX
PR   17-JUN-1998; 98JP-0188196.
XX
PR   26-JUN-1998; 98JP-0196729.
XX
PA   (NITSB ) JAPAN TOBACCO INC.
XX
WPI; 2000-286723/25.
XX
P-PSDB; AAY82611.
XX
PT   A human monoclonal antibody to parathyroid hormone related protein. -
PT   useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT   including metastasis, and pain
XX
PS   Example 10; Page 33-34; 88pp; Japanese.
XX
CC   The present invention describes a human monoclonal antibody to
CC   parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC   its fragments, following the stimulation of PTHrP has the following
CC   properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC   the release of calcium from bone; or (c) inhibits elevation of blood
CC   calcium content. The monoclonal antibody can be used in the treatment
CC   of hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC   metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC   diseases and gingiva, sepsis, systemic inflammatory response syndrome
CC   (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC   antiinflammatory activities. The present sequence represents a
CC   human PTHrP monoclonal antibody clone nucleotide sequence from the
CC   present invention.
XX
SQ   Sequence 720 BP; 174 A; 200 C; 187 G; 159 T; 0 other;

Query Match      77.5%; Score 269.6; DB 21; Length 720;
Best Local Similarity 85.9%; Pred. No. 1.6e-73;
Matches 299; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY   1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCCCTCC 60
DB   61 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCGGCCACC 120

QY   61 ATCTCTCTGCTCGCTCAGTAAAGAGTCTCTGTATAAGGATGGGAAGACATCTTGAATTGG 120

```


CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone nucleotide sequence from the
 CC present invention.

XX Sequence 720 BP; 169 A; 189 C; 190 G; 157 T; 15 other;

Query Match 77.0%; Score 267.8; DB 21; Length 720;
 Best Local Similarity 85.1%; Pred. No. 5.8e-73;
 Matches 296; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCCCTCC 60
 DB 61 GATATTGTGATGANTCAGTNTCCACTNNCTCCCTGCCGTCCACCCCTGGAGAGCGGCCCTCC 120
 QY 61 ATCTCTCTGCTCGCTAGAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
 DB 121 ATCTCTCTGCTCGCTAGAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 180
 QY 121 TACCTGCAAGACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACACCGGGCA 180
 DB 181 TACCTGCAAGACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGGTCTGATCGGGCC 240
 QY 181 TCAGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAATC 240
 DB 241 TCCGGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAATC 300
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 300
 DB 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 360
 QY 301 TTCAGTTCGGCCCAAGGACCAAGTGGAGATCAAAACGTTACGGTGGCT 348
 DB 361 TTCAGTTCGGCCCAAGGACCAAGTGGAGATCAAAACGTTACGGTGGCT 408

RESULT 14

AA13922
 ID AA13922 standard; DNA; 720 BP.

XX AC AA13922;

XX 02-AUG-2000 (first entry)

XX Human PTHrP monoclonal antibody clone IB3-9-16 DNA SEQ ID NO:7.

XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory; ds.

XX Homo sapiens.

XX JP2000080100-A.

XX 21-MAR-2000.

XX 12-OCT-1998; 98JP-0304793.

XX 17-JUN-1998; 98JP-0188196.

XX 26-JUN-1998; 98JP-0196729.

XX (NISB) JAPAN TOBACCO INC.

XX WPI: 2000-286723/25.

XX P-PSDB; AAY82612.

XX A human monoclonal antibody to parathyroid hormone related protein.

PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain

XX Example 10; Page 36-37; 88pp; Japanese.

XX The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
 CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone nucleotide sequence from the
 CC present invention.

XX Sequence 720 BP; 174 A; 190 C; 187 G; 166 T; 3 other;

Query Match 76.6%; Score 266.6; DB 21; Length 720;
 Best Local Similarity 85.1%; Pred. No. 1.4e-72;
 Matches 296; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCCCTCC 60
 DB 61 GATATTGTGATGANTCAGTNTCCACTCTCCCTGCCGTCCACCCCTGGAGAGCGGCCCTCC 120
 QY 61 ATCTCTCTGCTCGCTAGAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 120
 DB 121 ATCTCTCTGCTCGCTAGAGTCTCTGTATAGGATGGGAAGACATACCTTGAATTGG 180
 QY 121 TACCTGCAAGACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACACCGGGCA 180
 DB 181 TACCTGCAAGACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGGTCTGATCGGGCC 240
 QY 181 TCAGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAATC 240
 DB 241 TCCGGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTACACTGAAATC 300
 QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 300
 DB 301 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGTAGAGTATCCA 360
 QY 301 TTCAGTTCGGCCCAAGGACCAAGTGGAGATCAAAACGTTACGGTGGCT 348
 DB 361 TTCAGTTCGGCCCAAGGACCAAGTGGAGATCAAAACGTTACGGTGGCT 408

RESULT 15

AAF44895
 ID AAF44895 standard; cDNA; 963 BP.

XX AC AAF44895;

XX 28-MAR-2001 (first entry)

XX Human breast cancer related protein coding sequence SEQ ID NO: 51.

XX Human; breast cancer; diagnosis; therapy; vaccine; ss. i

XX Homo sapiens.

XX WO200078960-A2.

XX 28-DEC-2000.

XX 23-JUN-2000; 2000WO-US17536.

XX 23-JUN-1999; 99US-0140903.

XX 12-OCT-1999; 99US-0158980.

PA (CORI-) CORIXA CORP.
XX
PI Yugiou J, Mitcham JL;
XX
DR WPI; 2001-041426/05.
XX
PT New polynucleotides encoding breast tumor specific proteins, useful for
PT prevention, treatment and diagnosis of breast cancer -
XX
PS Claim 25; Page 135-136; 165pp; English.
XX
CC The present invention provides the coding sequences for a number of
CC breast cancer related proteins. These can be used in vaccinations
CC against, diagnosis of and treatment of cancer, particularly breast
CC cancer.
XX
SQ Sequence 963 BP; 253 A; 264 C; 224 G; 213 T; 9 other;
Query Match 75.68; Score 263.2; DB 22; Length 963;
Best Local Similarity 84.8%; Pred. No. 1.7e-71;
Matches 295; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCACCCCTGGAGAGCCGCCCTCC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
63 GATATTGTGATGACTCAGTCTCCACTCTCCAGCGCGTCACCCCTGGAGAGCCGCCCTCC 122
QY 61 ATCTCTGTGCGTGCAGTACAGTCTCTCTATAGGATGGGAAGACATACTTGAATTGG 120
Db |||||||| || ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
123 ATCTCTGCAAGTCTAGTCAGAGCTCTCTACATAGTAATGGATACAGTTATTGGATTGG 182
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCACCCGGGCA 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
183 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGGCTTTCTAAGCGGCC 242
QY 181 TCAGGGGTCCTGTACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db || ||||||||||||||||||||||||||||||||||||||||||||||||||||
243 TCCGGGTCCTGTACAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAGATC 302
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db || ||||||||||||||||||||||||||||||||||||||||||||||||||||
303 AGTAGAGTGGAGGCTGAGGATTTGGGTTTATTACTGTCAAACTCTACAGACCCCG 362
QY 301 TTCAGGTTGGCCAAAGGACCAAGGTGGAGATCAAAACGTACGGTGGCT 348
Db |||| |||||| ||||||||||||||||||||||||||||||||||||
363 CTCACCTTCGGCGGAGGACCAAGGTGGAGATCAAAACGAACCTGTGGCT 410
Search completed: April 26, 2003, 05:05:49
Job time : 74.0118 Secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 07:27:07 ; Search time 33 6331 Seconds
(without alignments)
11258.801 Million cell updates/sec

Title: US-09-674-716b-17

Perfect score: 348

Sequence: 1 gatatttgatgactcagtc.....agatcaaacgtacggtggct 348

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 709820 seqs, 544064369 residues

Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	263	75.6	1143	10	US-09-822-698A-6
2	262.8	75.5	339	10	US-09-822-698A-2
3	262.8	75.5	663	10	US-09-822-698A-25
4	256.8	73.8	968	9	US-09-924-340-7
5	256.8	73.8	968	9	US-09-992-600A-7
6	252	72.4	336	9	US-09-848-798-99
7	250.2	71.9	738	9	US-10-158-646-61
8	241.4	69.4	476	10	US-09-864-761-32306
9	241.4	69.4	563	10	US-09-864-761-15798
10	239.2	68.7	666	9	US-09-479-614-25
11	239.2	68.7	666	9	US-09-479-614-27
12	239.2	68.7	726	9	US-09-479-614-23
13	239.2	68.7	726	9	US-09-479-614-24
14	239.2	68.7	954	9	US-09-479-614-19
15	239.2	68.7	954	9	US-09-479-614-21
16	233	67.0	492	9	US-10-060-036-3813
17	231.6	66.6	375	10	US-09-753-436-65
18	228.6	65.7	344	10	US-09-840-459-98
19	228.6	65.7	344	10	US-09-840-459-105

ALIGNMENTS

RESULT 1

US-09-822-698A-6

; Sequence 6, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; PRIOR FILING DATE: 2001-03-30

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 6

; LENGTH: 1143

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: nucleotide sequence coding for amino acid sequence of

; OTHER INFORMATION: SEQ ID NO:5

US-09-822-698A-6

Query Match 75.6%; Score 263; DB 10; Length 1143;
Best Local Similarity 85.4%; Pred. No. 2,7e-78;
Matches 293; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 1 GATATTGATGACTCAGTCTCCACTCTCCCTGCCGCTGACCCCTGGAGAGCGGCGCTCC 60

Db 379 GAAATTGCTGACTCAGTCTCCACTCTCCCTGCCGCTGACCCCTGGAGAGCGGCGCTCC 438

Qy 61 ATCTCTCTCTCGCTCCAGTAAGAGTCTCTGTATAGGATGGAGACATATCTTAATTGG 120

Db 439 ATCTCTCTCGAGTCTTAGTCAGAGGCTCTCTGATATGATACATATTTGGATTGG 498

Qy 121 TACTTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGATGCTCCACCGGGCA 180

Db 499 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGATGCTCCACCGGGCC 558

Qy 181 TCAGGGGTCCTGACAGGTTTCAGTGGCAGTGGATGAGGCACAGATTTTACACTGAAATC 240

Db 181 TCAGGGGTCCTGACAGGTTTCAGTGGCAGTGGATGAGGCACAGATTTTACACTGAAATC 240

```
Db 559 TCCGGGGTCCCTGACAGGTTCCAGTGGCAGTGTATCAGGCACAGATTTTACACTGAGAAATC 618
Qy 241 AGCAGATGGAGGCTGAGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 619 AGCAGATGGAGGCTGAGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 678
Qy 301 TTCAGTTTCGGCCCAAGGACCAAGGTGGAGATCAAACTAGG 343
Db 679 TTCAGTTTCGGCCCTGGGACCAAGGTGGATATCAACAGGGG 721

RESULT 2
US-09-822-698A-2
; Sequence 2, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 2
; LENGTH: 339
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence coding for amino acid sequence of
US-09-822-698A-2
Query Match 75.5%; Score 262.8; DB 10; Length 339;
Best Local Similarity 86.1%; Pred. No. 2.1e-78;
Matches 291; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCTCCAGTCTCCACTCTCCCTGCCCTCACCCCTGGAGAGCGGCGCTCC 60
Db 1 GAAATTGTGCTGACTCAGTCTCCACTCTCCCTGCCCTCACCCCTGGAGAGCGGCGCTCC 60
Qy 61 ATCTCCTGCTCGCTGAGTAAAGTCTCTCTGTATAGGATGGGAACATCATTTGAATTGG 120
Db 61 ATCTCCTGAGGTCTAGTCAGAGCCCTCTCTGCATAGTAATGGATACACCTATTTTGGATTGG 120
Qy 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGCA 180
Db 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCATCGGGCC 180
Qy 181 TCAGGGTCTCCAGTTCAGTGGCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 240
Db 181 TCCGGGTCTCCAGTTCAGTGGCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 240
Qy 241 ACAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 241 ACAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Qy 301 TTCAGTTTCGGCCCAAGGACCAAGGTGGAGATCAAAAG 338
Db 301 TTCAGTTTCGGCCCTGGGACCAAGGTGGATATCAAAAG 338

RESULT 3
US-09-822-698A-25
; Sequence 25, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
```

```
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 25
; LENGTH: 663
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence coding for amino acid sequence of
US-09-822-698A-25
Query Match 75.5%; Score 262.8; DB 10; Length 663;
Best Local Similarity 86.1%; Pred. No. 2.7e-78;
Matches 291; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCTCCAGTCTCCACTCTCCCTGCCCTCACCCCTGGAGAGCGGCGCTCC 60
Db 1 GAAATTGTGCTGACTCAGTCTCCACTCTCCCTGCCCTCACCCCTGGAGAGCGGCGCTCC 60
Qy 61 ATCTCCTGCTCGCTGAGTAAAGTCTCTCTGTATAGGATGGGAACATCATTTGAATTGG 120
Db 61 ATCTCCTGAGGTCTAGTCAGAGCCCTCTCTGCATAGTAATGGATACACCTATTTTGGATTGG 120
Qy 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCACCCGGCA 180
Db 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGATGTCCATCGGGCC 180
Qy 181 TCAGGGTCTCCAGTTCAGTGGCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 240
Db 181 TCCGGGTCTCCAGTTCAGTGGCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 240
Qy 241 ACAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 241 ACAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Qy 301 TTCAGTTTCGGCCCAAGGACCAAGGTGGAGATCAAAAG 338
Db 301 TTCAGTTTCGGCCCTGGGACCAAGGTGGATATCAAAAG 338

RESULT 4
US-09-924-340-7
; Sequence 7, Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US2.REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 7
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..31
; NAME/KEY: CDS
```


;
; LOCATION: 32..748
; NAME/KEY: 3'UTR
; LOCATION: 749..968
; NAME/KEY: polyA_signal
; LOCATION: 928..933
; NAME/KEY: polyA_site
; LOCATION: 953..968
US-09-924-340-7

Query Match 73.8%; Score 256.8; DB 9; Length 968;
Best Local Similarity 83.6%; Pred. No. 3.1e-76;
Matches 291; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGCTCAGCCCTGGAGAGCGGCTCC 60
DB 92 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGCTCAGCCCTGGAGAGCGGCTCC 151
QY 61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATTAAGGATGGGAAGACATATCTTGAATTGG 120
DB 152 ATCTCCTGTCGCTCGAGTCAAGGCTCTCGATGTTCAAGGCTCCAACTATTTGGATTGG 211
QY 121 TACCTGCGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCGGGCA 180
DB 212 TACCACCAAGAGCCAGGCGAGTCTCCAACTCCTGATATATCTTGGTTCTTAATCGGGCC 271
QY 181 TCAGGGGTCCCTACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 272 TCCGGGTCCCTACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 331
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 332 AGTAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAACTCCA 391
QY 301 TTCAGGTTCCGCCAAGGACCAAGTGGAGATCAAACTAGGTGGCT 348
DB 392 TTCAGTTTCGGCCCTGGGACCAAGTGGATATCAAGCGAAGTGGCT 439

RESULT 5

US-09-992-600A-7
; Sequence 7, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephanie
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992,600A
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: JPatent
; SEQ ID NO 7
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..31
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..748

;
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 749..968
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 928..933
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 953..968
US-09-992-600A-7

Query Match 73.8%; Score 256.8; DB 9; Length 968;
Best Local Similarity 83.6%; Pred. No. 3.1e-76;
Matches 291; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGCTCAGCCCTGGAGAGCGGCTCC 60
DB 92 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGCTCAGCCCTGGAGAGCGGCTCC 151
QY 61 ATCTCCTGTCGCTCGAGTAAGAGTCTCCTGTATTAAGGATGGGAAGACATATCTTGAATTGG 120
DB 152 ATCTCCTGCGAGTCTAGTCAGAGCTCCTGATGTTCAAGGCTCCAACTATTTGGATTGG 211
QY 121 TACCTGCGAAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCGGGCA 180
DB 212 TACCACCAAGAGCCAGGCGAGTCTCCAACTCCTGATATATCTTGGTTCTTAATCGGGCC 271
QY 181 TCAGGGGTCCCTACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 272 TCCGGGTCCCTACAGGTTGAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 331
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 332 AGTAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAACTCCA 391
QY 301 TTCAGGTTCCGCCAAGGACCAAGTGGAGATCAAACTAGGTGGCT 348
DB 392 TTCAGTTTCGGCCCTGGGACCAAGTGGATATCAAGCGAAGTGGCT 439

RESULT 6

US-09-848-798-99
; Sequence 99, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain G01
US-09-848-798-99

Query Match 72.4%; Score 252; DB 9; Length 336;

Best Local Similarity 84.9%; Pred. No. 9e-75;
Matches 282; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 7 GTGATGACTCAGTCTCCACTCTCCCTGCCGCTCAGCCCTGGAGAGCGGCTCCATCTCC 66
DB 4 GAGCTCACTCAGTCTCCACTCTCCCTGCCGCTCAGCCCTGGAGAGCGGCTCCATCTCC 63

Qy 67 TGTCTGCTGAGTAAAGTCTCTCTATAGAGTGGGAAGACATATTGAATTGGTACCTG 126
Db 64 TGCAGGTCTAGTACAGAGCTCTCATAGTAGTGATTTTGGATTCACTTTTGGATTGGTACCTG 123
Qy 127 CAGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTTGTCACCCGGGATCAGG 186
Db 124 CAGAAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTGTTGTTCAATCGGCGCTCCGG 183
Qy 187 GTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCAGCAGA 246
Db 184 GTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCAGCAGA 243
Qy 247 GTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCATTCAAG 306
Db 244 GTGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATTCCTCACT 303
Qy 307 TTCGCGCAAGGCAACAGTGGAGATCAAAACG 338
Db 304 TTCGCGGAGGACCAAGTGGAGATCAAAACG 335

RESULT 7

US-10-158-646-61
; Sequence 61, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy K.W.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0030-1 US
; CURRENT APPLICATION NUMBER: US/10/158,646
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/295,239
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PERL Program
; SEQ ID NO 61
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030073105A1 1329931.2
US-10-158-646-61

Query Match 71.9%; Score 250.2; DB 9; Length 738;
Best Local Similarity 84.0%; Pred. No. 4.7e-74;
Matches 295; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTCGAGAGCGGCGCTCC 60
Db 81 GATATTGTGATGACCCAGACTCCACGCTCCCTGCCGTACCCCTCGAGAGCGGCGCTCC 140
Qy 61 ATCTCTGTCTCGTAGTAGTCTCTGTATA---AGGATGGGAAGACATATTGAAT 117
Db 141 ATCTCTGTGAGGCTAGTCAGAGCTCTCTGATAGTATGATGAAACACCTATTGGAC 200
Qy 118 TGGTACCTGACAGAGCAGGCGAGTCTCCACAGCTCTGATCTATTGATGCCACCGG 177
Db 201 TGGTACCTGACAGAGCAGGCGAGTCTCCACAGCTCTGATCTATTGATGCCACCGG 260
Qy 178 GCATCAGGGTCTCCAGAGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAA 237
Db 261 GCCTCTGAGTCCACAGAGTTTCAGTGGCAGTGGATCAGGCACACTAATTTACACTGAA 320
Qy 238 ATCAGCAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATAT 297
Db 321 ATCAGCAGGTTGAGGCTGACGATGTTGGAGTTTATTACTGCATGCAACGATAGATTT 380
Qy 298 CCATTACGTTCCGCCAAGGACCAAGTGGAGATCAACAGTACGGTGCT 348
Db 381 CCGTCACTTTCCGCGAGGACCAAGGTAGAGATCAACAGTACGTTGCT 431

RESULT 8

US-09-864-761-32306
; Sequence 32306, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32306
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP001224.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 18
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 14
; OTHER INFORMATION: EST_HUMAN HIT: AA464313.1, EVALUATE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P06309, EVALUATE 9.00e-55
; OTHER INFORMATION: NT HIT: X12691.1, EVALUATE 0.00e+00
US-09-864-761-32306

Query Match 69.4%; Score 241.4; DB 10; Length 476;
Best Local Similarity 85.4%; Pred. No. 3.7e-71;
Matches 269; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCGGCGCTCC 60
Db 12 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCGTACCCCTGGAGAGCGGCGCTCC 71

```
QY 61 ATCTCTCTGCTCGAGTAAAGACTCTCTGTATTAAGGATGGAGACACATACCTTGAATTGG 120
DB 72 ATCTCTCTGCTCGAGTAAAGACTCTCTGTATTAAGGATGGAGACACATACCTTGAATTGG 131
QY 121 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGATCTCCACCGGGCA 180
DB 132 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGATCTCCACCGGGCA 191
QY 181 TCAGGGTCTCTGACAGTTTCAAGTTCAGTGGGATGAGTGGGATGAGTGGGATGAGTGGG 240
DB 192 TCCGGGTCTCTGACAGTTTCAAGTTCAGTGGGATGAGTGGGATGAGTGGGATGAGTGGG 251
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTATTTACTGTCAACAGCTGGTGAAGTATCCA 300
DB 252 AGCAGAGTGGAGGCTGAGGATGTTGGGGTATTTACTGTCAACAGCTGGTGAAGTATCCA 311
QY 301 TTCAGGTTTCGGCCAA 315
DB 312 CCCACAGTGGGTACAA 326
```

RESULT 9

```
US-09-864-761-15798
; Sequence 15798, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
```

```
; SOFTWARE: Rnobox Sequence Listing Engine vers. 1.1
; SEQ ID NO 15798
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP001224.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 18
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 14
US-09-864-761-15798
```

```
Query Match 59.4%; Score 241.4; DB 10; Length 563;
Best Local Similarity 85.4%; Pred. No. 3.9e-71;
Matches 269; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCCCTGAGAGCGCGCTCC 60
DB 62 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCCCTGAGAGCGCGCTCC 121
QY 61 ATCTCTCTGCTCGAGTAAAGACTCTCTGTATTAAGGATGGAGACACATACCTTGAATTGG 120
DB 122 ATCTCTCTGCTCGAGTAAAGACTCTCTGTATTAAGGATGGAGACACATACCTTGAATTGG 181
QY 121 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGATCTCCACCGGGCA 180
DB 182 TACCTGAGAGCCAGGCGAGTCTCCACAGCTCTCTGATCTATTTGATCTCCACCGGGCA 241
QY 181 TCAGGGTCTCTGACAGTTTCAAGTTCAGTGGGATGAGTGGGATGAGTGGGATGAGTGGG 240
DB 242 TCCGGGTCTCTGACAGTTTCAAGTTCAGTGGGATGAGTGGGATGAGTGGGATGAGTGGG 301
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTATTTACTGTCAACAGCTGGTGAAGTATCCA 300
DB 302 AGCAGAGTGGAGGCTGAGGATGTTGGGGTATTTACTGTCAACAGCTGGTGAAGTATCCA 361
QY 301 TTCAGGTTTCGGCCAA 315
DB 362 CCCACAGTGGGTACAA 376
```

RESULT 10

```
US-09-479-614-25
; Sequence 25, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; CURRENT FILING DATE: 2000-01-07
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
US-09-479-614-25
```

```
Query Match 68.7%; Score 239.2; DB 9; Length 666;
Best Local Similarity 80.5%; Pred. No. 2.3e-70;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCCCTGAGAGCGCGCTCC 60
DB 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCGTCCACCCCTGAGAGCGCGCTCC 60
QY 61 ATCTCTCTGCTCGAGTAAAGACTCTCTGTATTAAGGATGGAGACACATACCTTGAATTGG 120
DB 61 ATCTCTCTGCTCGAGTAAAGACTCTCTGTATTAAGGATGGAGACACATACCTTGAATTGG 120
```

```

QY 121 TACCTGCAGAGCCAGCGGACAGCTCCACAGAGCTCCTGATCTATTGATGTCACCCCGGCA 180
Db 121 TACCTGCAGAGCCAGCGGACAGCTCCACAGAGCTCCTGATCTATTGATGTCACCCCGGAC 180
QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 240
Db 181 TCTGGGGTCCACAGACAGGTTTCAGTGGCAGTGGGTTCAGGACAGATTTTACACCTCAGATC 240
QY 241 ACCAGATGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 241 ACCAGGTTGGAGGCTGACGAGCTGGGTGTTATTACTGCGGTCAAGGTTTACAGCATCCT 300
QY 301 TTCACGTTTCGCCCAAGGACCAAGGTGGAGATCAAACTACCGTGGCT 348
Db 301 CTCACCTTTCCGCCCCAGGTACCAAGCTGGAGATCAAAACGGAGTGCT 348

```

```

RESULT 11
US-09-479-614-27/c
; Sequence 27, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Felis catus
US-09-479-614-27

```

```

Query Match 68.7%; Score 239.2; DB 9; Length 666;
Best Local Similarity 80.5%; Pred. No. 2.3e-70;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACCTCGAGAGCCGGCCTCC 60
Db 666 GATATTGTGATGAGCAGACCCCTCTGTCCCTGCTCCCTCGTCCAGCCCTGGAGAGCCAGCTCA 607
QY 61 ATCTCTCTGCTCGAGTAAGAGTCTCTGATAAGGATGGAGACATCTTGAATTGG 120
Db 606 ATCTCTCTGAGGCGCTCAGACCCCTCTGTACAGTGTGGAATCTTATCTGAATTGG 547
QY 121 TACCTGCAGAGCCAGCGGACAGCTCCACAGAGCTCCTGATCTATTGATGTCACCCCGGCA 180
Db 546 TACCTGCAGAGCCAGCGGACAGCTCCACAGCGCTTGTATCTATTGTTTCCAAACCGGGAC 487
QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 240
Db 486 TCTGGGGTCCACAGACAGGTTTCAGTGGCAGTGGGTTCAGGACAGATTTTACACCTCAGATC 427
QY 241 ACCAGATGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 426 ACCAGGTTGGAGGCTGACGAGCTGGGTGTTATTACTGCGGTCAAGGTTTACAGCATCCT 367
QY 301 TTCACGTTTCGCCCAAGGACCAAGGTGGAGATCAAACTACCGTGGCT 348
Db 366 CTCACCTTTCCGCCCCAGGTACCAAGCTGGAGATCAAAACGGAGTGCT 319

```

```

RESULT 12
US-09-479-614-23
; Sequence 23, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine

```

```

; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Felis catus
US-09-479-614-23

```

```

Query Match 68.7%; Score 239.2; DB 9; Length 726;
Best Local Similarity 80.5%; Pred. No. 2.3e-70;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACCTCGAGAGCCGGCCTCC 60
Db 61 GATATTGTGATGAGCAGACCCCTCTGTCCCTGCTCCCTCGTCCAGCCCTGGAGAGCCAGCTCA 120
QY 61 ATCTCTCTGCTCGAGTAAGAGTCTCTGATAAGGATGGAGACATCTTGAATTGG 120
Db 121 ATCTCTCTGAGGCGCTCAGACAGCTCCTGTACAGTGTGGAATCTTATCTGAATTGG 180
QY 121 TACCTGCAGAGCCAGCGGACAGTCTCCACAGAGCTCCTGATCTATTGATGTCACCCCGGCA 180
Db 181 TACCTGCAGAGCCAGCGGACAGTCTCCAGGCGCTTGTATCTATTGTTTCCAAACCGGGAC 240
QY 181 TCAGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 240
Db 241 TCTGGGTCCACAGACAGGTTTCAGTGGCAGTGGGTTCAGGACAGATTTTACACCTGAGAATC 300
QY 241 AGCAGATGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 301 AGCAGGTTGAGGCTGACAGCTCGGTGTTTATTACTCGGTCAAGGTTTACAGCATCCT 360
QY 301 TTCACGTTTCGCCCAAGGACCAAGGTGGAGATCAAACTACCGTGGCT 348
Db 361 CTCACCTTTCCGCCCCAGGTACCAAGCTGGAGATCAAAACGGAGTGCT 408

```

```

RESULT 13
US-09-479-614-24/c
; Sequence 24, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER FILING DATE: 2000-01-07
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Felis catus
US-09-479-614-24

```

```

Query Match 68.7%; Score 239.2; DB 9; Length 726;
Best Local Similarity 80.5%; Pred. No. 2.3e-70;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCCACCTCGAGAGCCGGCCTCC 60
Db 666 GATATTGTGATGAGCAGACCCCTCTGTCCCTGCTCCCTCGTCCAGCCCTGGAGAGCCAGCTCA 607

```

1

QY 61 ATCTCTCTCCTCGAGTAAAGAGTCTCCTGTATAGAGTGGGAAGACATACCTTGAATTGG 120
Db 606 ATCTCTCAGGGCCAGTCTGACAGCTCTCTGTACAGTGGAAATACCTATCTGAATTGG 547
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCCTCATCTATTTGATGTCCACCCGGGCA 180
Db 546 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCCTCATCTATCTTGTTCACACGGGAC 487
QY 181 TCAGGGGTCCTGCAGAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 486 TCTGGGGTCCACAGACAGTTCAGTGGCAGTGGGTACGGACAGATTTACCCCTGAGAATC 427
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTAAGTGTCAACAGCTGTAGAGTATCCA 300
Db 426 AGCAGAGTGGAGGCTGAGGATGTTTATTAAGTGTCAAGGTTTACAGCATCCT 367
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348
Db 366 CTCACATTTTCGGCCAGGTACCAAGCTGGAGATCAACAGGAGTATGCT 319

RESULT 14
US-09-479-614-19
; Sequence 19, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Fells catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(732)
; FEATURE:
US-09-479-614-19

Query Match 68.7%; Score 239.2; DB 9; Length 954;
Best Local Similarity 80.5%; Pred. No. 2.5e-70;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCTGCTCCCTGACCCCTGAGAGCGGCTCC 60
Db 67 GATATTGTGATGACCGACAGCCCTCTGTCCCTGTCCCTGACCCCTGAGAGCGGCTCA 126
QY 61 ATCTCTCTGCTCGAGTAAAGAGTCTCCTGTATAGAGTGGGAAGACATACCTTGAATTGG 120
Db 127 ATCTCTGAGGCGGCGAGTCTGACAGCTCTCTGTACAGTGGTAAATACCTTGAATTGG 186
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCCTCATCTATTTGATGTCCACCCGGGCA 180
Db 187 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCCTCATCTTGTTCACACGGGAC 246
QY 181 TCAGGGGTCCTGCAGAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 247 TCTGGGGTCCACAGACAGTTCAGTGGCAGTGGGTACGGACAGATTTACCCCTGAGAATC 306
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTAAGTGTCAACAGCTGTAGAGTATCCA 300
Db 307 AGCAGAGTGGAGGCTGAGGATGTTTATTAAGTGTCAAGGTTTACAGCATCCT 366
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348
Db 367 CTCACATTTTCGGCCAGGTACCAAGCTGGAGATCAACAGGAGTATGCT 414

RESULT 15
US-09-479-614-21/c
; Sequence 21, Application US/09479614
; Publication No. US20030013183A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine
; APPLICANT: Weber, Eric
; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
; FILE REFERENCE: P-1047
; CURRENT APPLICATION NUMBER: US/09/479,614
; EARLIER APPLICATION NUMBER: 60/115,033
; EARLIER FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Fells catus
US-09-479-614-21

Query Match 68.7%; Score 239.2; DB 9; Length 954;
Best Local Similarity 80.5%; Pred. No. 2.5e-70;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCTGCTCCCTGACCCCTGAGAGCGGCTCC 60
Db 888 GATATTGTGATGACCGACAGCCCTCTGTCCCTGTCCCTGACCCCTGAGAGCGGCTCA 829
QY 61 ATCTCTCTGCTCGAGTAAAGAGTCTCCTGTATAGAGTGGGAAGACATACCTTGAATTGG 120
Db 828 ATCTCTGAGGCGGCGAGTCTGACAGCTCCTGTACAGTGGTAAATACCTTGAATTGG 769
QY 121 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCCTCATCTATTTGATGTCCACCCGGGCA 180
Db 768 TACCTGCAGAACCCAGGCGAGTCTCCACAGCTCCTCATCTTGTTCACACGGGAC 709
QY 181 TCAGGGGTCCTGCAGAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 708 TCTGGGGTCCACAGACAGTTCAGTGGCAGTGGGTACGGACAGATTTACCCCTGAGAATC 649
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTAAGTGTCAACAGCTGTAGAGTATCCA 300
Db 648 AGCAGAGTGGAGGCTGAGGATGTTTATTAAGTGTCAAGGTTTACAGCATCCT 589
QY 301 TTCAGTTCGGCCAGGACCAAGTGGAGATCAACAGTACGGTGGCT 348
Db 588 CTCACATTTTCGGCCAGGTACCAAGCTGGAGATCAACAGGAGTATGCT 541

Search completed: April 26, 2003, 09:24:13
Job time : 37.6331 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:57:16 ; Search time 14.4142 seconds
(without alignments)
7404.053 Million cell updates/sec

Title: US-09-674-716B-17

Perfect score: 348

Sequence: 1 gatattgtgatgactcagtc.....agatcaaacgtacgggtggct 348

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261.2	75.1	339	1 US-08-082-623-2	Sequence 2, Appli
2	252.8	72.6	336	3 US-09-000-088-1	Sequence 1, Appli
3	252	72.4	336	4 US-09-240-274-99	Sequence 99, Appl
4	249.4	71.7	339	1 US-08-264-093-9	Sequence 9, Appli
5	244	70.1	420	4 US-09-214-0950-111	Sequence 111, App
6	244	70.1	464	1 US-08-438-123-15	Sequence 15, Appl
7	243.6	70.0	339	2 US-08-672-345C-88	Sequence 88, Appl
8	243.6	70.0	339	4 US-09-214-0950-99	Sequence 99, Appl
9	240.4	69.1	368	2 US-08-672-345C-86	Sequence 86, Appl
10	240.4	69.1	368	4 US-09-214-0950-107	Sequence 107, App
11	239.2	68.7	368	2 US-08-672-345C-90	Sequence 90, Appl
12	239.2	68.7	368	4 US-09-214-0950-103	Sequence 103, App
13	238.8	68.6	339	4 US-09-406-532-13	Sequence 13, Appl
14	231.6	66.6	375	1 US-08-482-882-65	Sequence 65, Appl
15	231.6	66.6	375	1 US-08-483-389-65	Sequence 65, Appl
16	231.6	66.6	375	2 US-08-487-113D-65	Sequence 65, Appl
17	231.6	66.6	375	2 US-08-473-503-65	Sequence 65, Appl
18	231.6	66.6	375	2 US-08-483-932-65	Sequence 65, Appl
19	231.6	66.6	375	2 US-08-720-420A-65	Sequence 65, Appl
20	231.6	66.6	375	3 US-08-714-017-65	Sequence 65, Appl
21	231.6	66.6	375	3 US-08-475-680-65	Sequence 65, Appl
22	228.8	65.7	336	3 US-08-483-749A-3	Sequence 3, Appli
23	227.4	65.3	373	3 US-08-732-708C-40	Sequence 40, Appl
24	226	64.9	399	1 US-08-253-877C-9	Sequence 9, Appli
25	226	64.9	399	2 US-08-452-164A-9	Sequence 9, Appli
26	226	64.9	399	3 US-08-603-024-3	Sequence 3, Appli
27	225.2	64.7	882	1 US-08-392-419-3	Sequence 3, Appli

28 224.8 64.6 720 3 US-08-487-550-5 Sequence 5, Appli

29 222.2 63.9 1095 3 US-08-875-811-52 Sequence 52, Appl

30 222.2 63.9 1098 3 US-08-875-811-54 Sequence 54, Appl

31 221.2 63.6 405 1 US-08-259-372A-11 Sequence 11, Appl

32 221.2 63.6 405 1 US-08-468-671-11 Sequence 11, Appl

33 218.6 62.8 394 1 US-07-977-696C-64 Sequence 64, Appl

34 218.6 62.8 394 1 US-08-129-930B-64 Sequence 64, Appl

35 218.6 62.8 394 4 US-08-976-288A-64 Sequence 64, Appl

36 215.6 62.0 325 1 US-08-468-661-4 Sequence 4, Appli

37 215.6 62.0 325 1 US-08-466-272A-4 Sequence 4, Appli

38 215.6 62.0 325 1 US-08-478-857-4 Sequence 4, Appli

39 215.6 62.0 325 2 US-08-471-771-4 Sequence 4, Appli

40 215.6 62.0 325 3 US-09-130-783-4 Sequence 4, Appli

41 215.2 61.8 427 1 US-08-053-171-8 Sequence 8, Appli

42 214.2 61.6 749 4 US-08-983-035A-46 Sequence 46, Appl

43 214.2 61.6 1611 4 US-08-983-035A-37 Sequence 37, Appl

44 213.8 61.4 394 1 US-08-129-930B-93 Sequence 93, Appl

45 213.8 61.4 394 4 US-08-134-346A-48 Sequence 48, Appl

ALIGNMENTS

RESULT 1

US-08-082-623-2

; Sequence 2, Application US/08082623

; Patent No. 5750106

; GENERAL INFORMATION:

; APPLICANT: Ostberg, Lars G.

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO

; TITLE OF INVENTION: CYTOMEGALOVIRUS

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/082,623

; FILING DATE: 25-JUN-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/010,228

; FILING DATE: 28-JAN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, William M.

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 11823-055-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 339 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: 1..339

; OTHER INFORMATION: /standard_name= "Nucleotide

; OTHER INFORMATION: Sequence of the V-1 region of SDZ MSL 109"

; Patent No. 5750106

US-08-082-623-2

Query Match 75.1%; Score 261.2; DB 1; Length 339;
Best Local Similarity 85.8%; Pred. No. 6.6e-75;
Matches 290; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGCGCTCC 60
Db 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGCGCTCC 60
QY 61 ATCTCCTCTCGCTCGAGTAAGAGTCTCTGTATTAAGATGGAGACATACCTTGAATTGG 120
Db 61 ATCTCCTCGAGTCTAGTCAGAGCTCTCTGATACATAATGATACAACTATTGGATTGG 120
QY 121 TACGTGCAAGAGCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCCGGGCA 180
Db 121 TACGTGCAAGAGCAGGCGAGTCTCCACAGCTCCTGATCTATTCTGGCTTCTAATCGGGC 180
QY 181 TCAGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 181 TCCGGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 241 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTATGATGCAAGCTCTACAAATCCT 300
QY 301 TTCAGTTCGCCCAAGGACCAAGGTGGAGATCAACG 338
Db 301 CGGACGTTCCGCCAAGGACCAAGGTGGAATCAACG 338

RESULT 2

US-09-000-088-1
; Sequence 1, Application US/09000088
; Patent No. 6146629
; GENERAL INFORMATION:
; APPLICANT: DAGAN, Shlomo
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST HEPATITIS B VIRUS
; TITLE OF INVENTION: SURFACE ANTIGEN (HBVSA9)
; FILE REFERENCE: DAGAN-1
; CURRENT APPLICATION NUMBER: US/09/000,088
; CURRENT FILING DATE: 1998-01-22
; EARLIER APPLICATION NUMBER: PCT/IL97/00183
; EARLIER FILING DATE: 1997-06-10
; EARLIER APPLICATION NUMBER: IL96/118626
; EARLIER FILING DATE: 1996-06-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 336
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(336)
US-09-000-088-1

Query Match 72.6%; Score 252.8; DB 3; Length 336;
Best Local Similarity 84.5%; Pred. No. 3.4e-72;
Matches 284; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGCGCTCC 60
Db 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGCGCTCC 60
QY 61 ATCTCCTCTCGCTCGAGTAAGAGTCTCTGTATTAAGATGGGAAGACATCTTGAATTGG 120
Db 61 ATCTCCTCGCAGGCTAGTCAGAGCTCTCTGATAGTCTGGAACACACTATTGGATTGG 120
QY 121 TACGTGCAAGAGCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCCACCGGGCA 180
Db 121 TACGTGCAAGAGCAGGCGAGTCTCCACAGCTCCTGATCTATTGTTGGTTCTAATCGGGC 180

QY 181 TCAGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
Db 181 TCCGGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
Db 241 AGTAGAGTGGAGGCTGAGGATTTGGGGTTTATTACTGTCATGCAAGCTCTACAAATCCT 300
QY 301 TTCACCTTCGGCCCAAGGACCAAGGTGGAGATCAAA 336
Db 301 CGGACTTTTGGCCAGGGGACCAAGCTGGAGATCAAA 336

RESULT 3

US-09-240-274-99
; Sequence 99, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain G01
US-09-240-274-99

Query Match 72.4%; Score 252; DB 4; Length 336;
Best Local Similarity 84.9%; Pred. No. 6.1e-72;
Matches 282; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 7 GTGATGACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGCGCTCCATCTCC 66
Db 4 GAGCTCACTCAGTCTCCACTCTCCCTGCCCTGACCCCTGGAGAGCGCGCTCCATCTCC 63
QY 67 TCTCGCTCAGTAAGAGTCTCTCTGTATAAGGATGGAAGACATACTTCAATTGGTACCTG 126
Db 64 TCCAGGTCTAGTCAGAGCTCTCTGATAGTAGTGAATTCACATTTTGGATTGGTACCTG 123
QY 127 CAGAACCCAGGCGAGTCTCCACAGCTCCTGATCTATTTGATGTCCACCCGGGCATCAGG 186
Db 124 CAGAACCCAGGCGAGTCTCCACAGCTCCTGATCTATATGGTTCTTAATCGGCTCCGG 183
QY 187 GTCCCTGACAGGTTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCAGAGA 246
Db 184 GTCCCTGACAGGTTTCACTGGCAGTGGATCAGGCACAGATTTTACACTGAAATCAGAGA 243
QY 247 GTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCATTACG 306
Db 244 GTGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCATTACG 303
QY 307 TTCGCCCAAGGACCAAGGTGGAGATCAACG 338
Db 304 TTCGCCGAGGACCAAGGTGGAGATCAACG 335

RESULT 4

US-08-264-093-9
; Sequence 9, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan

;; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
;; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
;; TITLE OF INVENTION: ANTIGEN
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Ridout & Maybee
;; STREET: 2300 Richmond-Adeleide Centre
;; CITY: Toronto
;; STATE: Ontario
;; COUNTRY: Canada
;; ZIP: M5H 2J7
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: MS-DOS 6.00
;; SOFTWARE: ASCII Editor
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/264,093
;; FILING DATE:
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA: No. 5639863 applicable
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lake, James R.
;; REGISTRATION NUMBER: 31081
;; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (416) 868-1482
;; TELEFAX: (416) 362-0823
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 339 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single stranded
;; TOPOLOGY: linear
;; US-08-264-093-9

Query Match 71.7%; Score 249.4; DB 1; Length 339;
Best Local Similarity 85.5%; Pred. No. 4.2e-71;
Matches 290; Conservative 0; Mismatches 46; Indels 3; Gaps 1;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCCTGAGAGCGCGCTCC 60
DB 1 GATATTGTGATGACCCAGACTCCACTCTCCCTGCGCCCTGAGAGCGCGCTCC 60
QY 61 ATCTCCTGCTCGAGTAAAGTCTCTGTATA---AGGATGGGAAGACATCTTGAAT 117
DB 61 ATCTCCTGAGGTCTAGTCAGAGCTCTTGATAGTATGATGGAACACCTATTGGAC 120
QY 118 TGGTACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCCGG 177
DB 121 TGGTACCTGCAGAGCCAGGCGAGTCTCCACAGCTCCTGATCTATTGATGTCACCG 180
QY 178 GCATCAGGGTCCCTGACAGGTTGAGTGGCAGTGCAGGCACAGATTTACACTCAA 237
DB 181 GCCTGTGAGTCCAGAGGTTGAGTGGCAGTGCAGGCTGATGATTTACACTCAA 240
QY 238 ATCAGCAGTGGAGGCTGAGGATGTTGGGTTTATTACTGCAACAGCTGGTAGATAT 297
DB 241 ATCAGCAGGTTGAGGCTGAGGATGTTGGAGTTTATTACTGCAACAGCTGATAGATT 300
QY 298 CAATTCAGTTGGCGAAGGACCAAGGTGGAGATCAA 336
DB 301 CCTTCACTTTCGGGGAGGACCAAGGTGGAGATCAA 339

RESULT 5
US-09-214-095D-111
; Sequence 111, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

;; FILE REFERENCE: 51400-A-PCT-US
;; CURRENT APPLICATION NUMBER: US/09/214,095D
;; CURRENT FILING DATE: 1999-07-19
;; NUMBER OF SEQ ID NOS: 121
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 111
;; LENGTH: 420
;; TYPE: DNA
;; ORGANISM: Murine
;; FEATURE:
;; NAME/KEY: V-segment
;; LOCATION: (1)..(403)
;; OTHER INFORMATION: n at any position represents any nucleotide including c.g.t.a,
US-09-214-095D-111

Query Match 70.1%; Score 244; DB 4; Length 420;
Best Local Similarity 81.3%; Pred. No. 2.5e-69;
Matches 283; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCCTGAGAGCGCGCTCC 60
DB 53 GATATTGTGATGACCGCAGGATCACTCTCCAATCCTGTCACTTCTGGAGAATCAGTTTCC 112
QY 61 ATCTCCTGCTCGAGTAAAGTCTCTGTATAAGGATGGAGACATCTTGAATTGG 120
DB 113 ATCTCCTGAGGTCTAGTAGGAGTCTCTATATAGGATGGAGACATCTTGAATTGG 172
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGATCTCCACCGGGCA 180
DB 173 TTTCTGCGAGACAGGAGGATCTCTCACTCTGATCTATTGATCTCCACCGGTGCA 232
QY 181 TCAGGGTCCCTGACAGGTTTCACTGCGAGTGCAGTGCAGGCAGGATTTTACACTGAAAATC 240
DB 233 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGGTGAGTGGTGTATTACTGTCAACACTTTGTAGACTATCCA 292
QY 241 ACAGAGTGGAGGCTGAGGATGTTGGGTTTATTACTGTCAACACTGGTAGACTATCCA 300
DB 293 AGTAGAGTGAAGGCTGAGGATGTTGGTGTATTACTGTCAACACTTTGTAGACTATCCA 352
QY 301 TTCACCTTCGGCCAGGACCAAGGTGGAGATCAAAACGTACCGTGGCT 348
DB 353 TTCACCTTCGGCTCGGGACAAAGTTGGAGATAAAACGGGTTGATGCT 400

RESULT 6
US-08-438-123-15
; Sequence 15, Application US/08438123
; Patent No. 5552293
; GENERAL INFORMATION:
; APPLICANT: Lindholm et al
; TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,123
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/906,350
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: J.G. Mullins

REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 149-011
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 base pairs
TYPE: Nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-438-123-15

Query Match 70.1%; Score 244; DB 1; Length 464;
Best Local Similarity 81.3%; Pred. No. 2.6e-69;
Matches 283; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCCGGCCCTCC 60
DB 102 GATATTGTGATGACTCCAGTCTCCAGTCTCCCTGACCTCTGACCTCTCTGGAGAGTCAATCC 161
QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCTCTGTATAGGATGGGAACATATCTTGAATTGG 120
DB 162 ATCTCTGTCAGGTCTAGTAAAGTCTCTCTGTATAGGATGGGAACATATCTTGAATTGG 221
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTCTGATCTATTGATGTCACCCGGGCA 180
DB 222 TTCTCTGAGAGCCAGGCGAGTCTCTCTGATCTGATATATCGGATGTCACACCTTGTG 281
QY 181 TCAGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGCAGACAGATTTTACACTGAAATC 240
DB 282 TCAGGAGTCCGACAGAGTTCAGTGGCAGTGGATCAGGAGTCTCTTACACTGAGATC 341
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 342 AGTAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCTGCAACATCTAGAGTATCCG 401
QY 301 TTCACGTTCCGCGACAGGACCAAGGTGGAGATCAACGTCACGGTGGCT 348
DB 402 TTCACGTTCCGCGACAGGACCAAGGTGGAGATCAACGTCACGGTGGCT 449

RESULT 7

US-08-672-345C-88
Sequence 88, Application US/08672345C
Patent No. 5948558

GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672.345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 88:

SEQUENCE CHARACTERISTICS:
LENGTH: 339 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-672-345C-88

Query Match 70.0%; Score 243.6; DB 2; Length 339;
Best Local Similarity 82.5%; Pred. No. 3.1e-69;
Matches 279; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCCGGCCCTCC 60
DB 1 GATATTGTGATGACTCCAGTCTCCAGTCTCCCAATCTCTGATCTCTGGAGATCAATGTTCC 60
QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCTCTGTATAAGGATGGGAACATATCTTGAATTGG 120
DB 61 ATCTCTGTCAGGTCTAGTAGGAGTCTCTCTATATAGGATGGGAACATATCTTGAATTGG 120
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGATGTCACCCGGGCA 180
DB 121 TTCTCTGAGAGCCAGGCGAGTCTCTCAACTCTCTGATCTATTGATGTCACCCGGTCA 180
QY 181 TCAGGGTCCCTGACAGTTCAGTGGCAGTGGATCAGGCAGACAGATTTTACACTGAAATC 240
DB 181 TCAGGAGTCTCAGACCGGTTTAGTGGCAGTGGTTCAGGAACAGATTTTACCCCTGAAATC 240
QY 241 AGCAGAGTGGAGCTGAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
DB 241 AGTAGAGTGAAGGAGTGGGTTTATTACTGTCAACAGCTGGTAGAGTATCCA 300
QY 301 TTCACGTTCCGCGACAGGACCAAGGTGGAGATCAACG 338
DB 301 TTCACGTTCCGCGACAGGACCAAGGTGGAGATCAACG 338

RESULT 8

US-09-214-095D-99
Sequence 99, Application US/09214095D
Patent No. 6280987

GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patent in version 3.0
SEQ ID NO 99
LENGTH: 339
TYPE: DNA
ORGANISM: Murine
US-09-214-095D-99

Query Match 70.0%; Score 243.6; DB 4; Length 339;
Best Local Similarity 82.5%; Pred. No. 3.1e-69;
Matches 279; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCCAGTCTCCACTCTCCCTGCCCCGTCACCCCTGGAGAGCCGGCCCTCC 60
DB 1 GATATTGTGATGACTCCAGTCTCCCAATCTCTGATCTCTGGAGATCAATGTTCC 60
QY 61 ATCTCTGTCGCTCGAGTAAAGTCTCTCTGTATAAGGATGGGAACATATCTTGAATTGG 120
DB 61 ATCTCTGTCAGGTCTAGTAGGAGTCTCTCTATATAGGATGGGAACATATCTTGAATTGG 120
QY 121 TACCTGCAGAGCCAGGCGAGTCTCCACAGTCTCTGATCTATTGATGTCACCCGGGCA 180
DB 121 TTCTCTGAGAGCCAGGCGAGTCTCTCAACTCTCTGATCTATTGATGTCACCCGGTCA 180
QY 181 TCAGGGTCCCTGACAGGTTTACGTCAGTGGCAGTGGATCAGGCAGACAGATTTTACACTGAAATC 240

```

Db 181 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGTCCAGGACAGATTTCACCCCTGGAAATC 240
QY 241 AGCAGAGTGGAGGCTCAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 241 AGTAGAGTGAAGGCTCAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
QY 301 TTCACGTTCCGCCCAAGGCAAGGTTGGAGATCAAAAG 338
Db 301 TTCACGTTCCGCCCGCGGCAAAAGTTGGAGATAAAAG 338

RESULT 9
US-08-672-345C-86
; Sequence 86 Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 368 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-672-345C-86

Query Match 69.1%; Score 240.4; DB 2; Length 368;
Best Local Similarity 82.0%; Pred. No. 3.4e-68;
Matches 277; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCTCCACTCTCCCTGCGCGTCCACCCCTGGAGAGCCGGCCTCC 60
Db 1 GATATGGTGTGATGACGCAAGCACTCTCCATCTCTGTCACCTCTCTGGAGAATCAGTTTCC 60
QY 61 ATCTCCTGCTCGTCCAGTAAAGAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
Db 61 ATCTCCTGCGAGGTCTAGTAAGAGTCTCTATATAGGATGGGAAGACATCTTGAATTGG 120
QY 121 TACCTGCAGAGGACGAGGAGTCTCCAGCTCTCTGATCTATTGATGTCACCCGGCA 180
Db 121 TTCTGTCAGAGACGAGGACAACTCTCTCACCCTCTCTGATCTATTGATGTCACCCGGCA 180
QY 181 TCAGGGTCTCCCTGACAGAGTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 240
Db 181 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGTTCAGGACAGATTTTACCCCTGGAATC 240
QY 241 AGCAGAGTGGAGGCTCAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 241 AGTAGAGTGAAGGCTCAGGATGTTGGGTTTATTACTGTCAACATTTTGTAGATATCCA 300
QY 301 TTCACGTTCCGCCCAAGGCAAGGTTGGAGATCAAAAG 338
Db 301 TTCACGTTCCGCCCGCGGCAAAAGTTGGAGATAAAAG 338

RESULT 11
US-08-672-345C-90
; Sequence 90 Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

Db 241 AGTAGAGTGAAGGCTCAGGATGTTGGGTTTATTACTGTCAACATTTGTAGATATCCA 300
QY 301 TTCACGTTCCGCCCAAGGCAAGGTTGGAGATCAAAAG 338
Db 301 TTCACGTTCCGCCCGCGGCAAAAGTTGGAGATAAAAG 338

RESULT 10
US-09-214-095D-107
; Sequence 107 Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 368
; TYPE: DNA
; ORGANISM: Murine
US-09-214-095D-107

Query Match 69.1%; Score 240.4; DB 4; Length 368;
Best Local Similarity 82.0%; Pred. No. 3.4e-68;
Matches 277; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCTCCACTCTCCCTGCGCGTCCACCCCTGGAGAGCCGGCCTCC 60
Db 1 GATATGGTGTGATGACGCAAGCACTCTCCATCTCTGTCACCTCTCTGGAGAATCAGTTTCC 60
QY 61 ATCTCCTGCTCGTCCAGTAAAGAGTCTCTGTATAGGATGGGAAGACATCTTGAATTGG 120
Db 61 ATCTCCTGCGAGGTCTAGTAAGAGTCTCTATATAGGATGGGAAGACATCTTGAATTGG 120
QY 121 TACCTGCAGAGGACGAGGAGTCTCCAGCTCTCTGATCTATTGATGTCACCCGGCA 180
Db 121 TTCTGTCAGAGACGAGGACAACTCTCTCACCCTCTCTGATCTATTGATGTCACCCGGCA 180
QY 181 TCAGGGTCTCCCTGACAGAGTTCAGTGGCAGTGGATCAGGACAGATTTTACACTGAAATC 240
Db 181 TCAGGAGTCTCAGACCGGTTAGTGGCAGTGGTTCAGGACAGATTTTACCCCTGGAATC 240
QY 241 AGCAGAGTGGAGGCTCAGGATGTTGGGTTTATTACTGTCAACAGCTGGTAGATATCCA 300
Db 241 AGTAGAGTGAAGGCTCAGGATGTTGGGTTTATTACTGTCAACATTTTGTAGATATCCA 300
QY 301 TTCACGTTCCGCCCAAGGCAAGGTTGGAGATCAAAAG 338
Db 301 TTCACGTTCCGCCCGCGGCAAAAGTTGGAGATAAAAG 338

RESULT 11
US-08-672-345C-90
; Sequence 90 Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-672-345C-90

Query Match 68.7%; Score 239.2; DB 2; Length 368;
Best Local Similarity 80.5%; Pred. No. 8.3e-68;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCCGGCCTCC 60
DB 1 GATATGGTATGACGCAAGATGAACCTCCAATCTCTGTCACCTTCTGGAGAAATCAGTTTCC 60
QY 61 ATCTCTCTGCTCGAGTAAAGAGTCTCTGTATTAAGGATGGAGACATATCTTCAATTGG 120
DB 61 ATCTCTCGAGGTCTAGTAGGAGTCTCTATATAGGATGGAGACATATCTTCAATTGG 120
QY 121 TACTCTCAGAAGCCAGGGCAGTCTCCACAGCTCCCTGATCTATTGATCTCCACCGGGCA 180
DB 121 TTCTCTCAGAGCCAGGAGGATCTCTCACTCTCTGATCTATTGATCTCCACCGGGCA 180
QY 181 TCAGGGTCCCTGACAGGTTTCAAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 181 TCAGGAGTCTCAGACCCGGTTAGTGGCAGTGGTTCAGGACAGATTTTCACTTGAAGACTATCCA 300
QY 301 TTCACGTTCCGGCCAGGGACCAAGCTGGAGATCAAACTAGCGTGGCT 348
DB 301 TTCACGTTCCGGCTCGGGACAAAATTTGGAGATAAAACGGGCTGATGCT 348

RESULT 12
US-09-214-095D-103
Sequence 103, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
SEQ ID NO 103
LENGTH: 368
TYPE: DNA
ORGANISM: MURINE
US-09-214-095D-103

Query Match 68.7%; Score 239.2; DB 4; Length 368;
Best Local Similarity 80.5%; Pred. No. 8.3e-68;
Matches 280; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCCGGCCTCC 60
DB 1 GATATGGTATGACGCAAGATGAACCTCCAATCTCTGTCACCTTCTGGAGAAATCAGTTTCC 60
QY 61 ATCTCTCTGCTCGAGTAAAGAGTCTCTGTATTAAGGATGGAGACATATCTTCAATTGG 120
DB 61 ATCTCTCGAGGTCTAGTAGGAGTCTCTATATAGGATGGAGACATATCTTCAATTGG 120
QY 121 TACTCTCAGAAGCCAGGGCAGTCTCCACAGCTCCCTGATCTATTGATCTCCACCGGGCA 180
DB 121 TTCTCTCAGAGCCAGGAGGATCTCTCACTCTCTGATCTATTGATCTCCACCGGGCA 180
QY 181 TCAGGGTCCCTGACAGGTTTCAAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 181 TCAGGAGTCTCAGACCCGGTTAGTGGCAGTGGTTCAGGACAGATTTTCACTTGAAGACTATCCA 300
QY 301 TTCACGTTCCGGCCAGGGACCAAGCTGGAGATCAAACTAGCGTGGCT 348
DB 301 TTCACGTTCCGGCTCGGGACAAAATTTGGAGATAAAACGGGCTGATGCT 348

RESULT 13
US-09-406-532-13
Sequence 13, Application US/09406532A
Patent No. 6365154
GENERAL INFORMATION:
APPLICANT: Connie L. Erickson-Miller
APPLICANT: Stephen D. Holmes
APPLICANT: James D. Winkler
TITLE OF INVENTION: TIE2 Agonist Antibodies
FILE REFERENCE: P50843
CURRENT APPLICATION NUMBER: US/09/406,532A
CURRENT FILING DATE: 1999-09-27
PRIOR APPLICATION NUMBER: 60/102,098
PRIOR FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 339
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(339)
OTHER INFORMATION: 13h10 light chain v region
US-09-406-532-13

Query Match 68.6%; Score 238.8; DB 4; Length 339;
Best Local Similarity 81.7%; Pred. No. 1.1e-67;
Matches 276; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 1 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCGCCGTCACCCCTGGAGAGCCGGCCTCC 60
DB 1 GATATCGTATGACTCAGGCTCAGTCTCTGTACCTGTCACCTCTCTGGAGAGTCAAGTATCC 60
QY 61 ATCTCTCTGCTCGAGTAAAGAGTCTCTGTATTAAGGATGGAGACATATCTTCAATTGG 120
DB 61 ATCTCTCGAGGTCTAGTAGTATCTCTGTCATAGAAATGGCAACACTTACTTGTATTTGG 120
QY 121 TACTCTCAGAAGCCAGGGCAGTCTCCACAGCTCCCTGATCTATTGATCTCCACCGGGCA 180
DB 121 TTCTCTCAGAGCCAGGAGGAGTCTCTCAGCTCTCTGATATATATCGATCTCCAACTTGGC 180
QY 181 TCAGGGTCCCTGACAGGTTTCAAGTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAATC 240
DB 181 TCAGGAGTCTCAGACAGGTTTCAAGTTCAGTGGGTCAGGAACTGCTTTTCCACTGAGAATC 240
QY 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGAGTATATCCA 300
DB 241 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGTCAACAGCTGAGTATATCCA 300

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:53:31 ; Search time 2664.21 Seconds
(without alignments)
14583.043 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 1335

Sequence: 1 gaggtgcagctgtggagtc.....ccctgtctccgggtaaatga 1335

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:**

1: gb_ba:**

2: gb_htg:**

3: gb_in:**

4: gb_om:**

5: gb_ov:**

6: gb_pat:**

7: gb_ph:**

8: gb_pl:**

9: gb_pr:**

10: gb_ro:**

11: gb_sts:**

12: gb_sy:**

13: gb_un:**

14: gb_vi:**

15: em_ba:**

16: em_fun:**

17: em_hum:**

18: em_in:**

19: em_mu:**

20: em_om:**

21: em_or:**

22: em_ov:**

23: em_pat:**

24: em_ph:**

25: em_pl:**

26: em_ro:**

27: em_sts:**

28: em_un:**

29: em_vi:**

30: em_htg_hum:**

31: em_htg_inv:**

32: em_htg_other:**

33: em_htg_mus:**

34: em_htg_pln:**

35: em_htg_rod:**

36: em_htg_mam:**

37: em_htg_vrt:**

38: em_sy:**

39: em_htgo_hum:**

40: em_htgo_mus:**

41: em_htgo_other:**

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1335	100.0	1335	6	AX010615	AX010615 Sequence
2	1335	100.0	1335	6	AX010646	AX010646 Sequence
3	1156	85.6	1679	9	BC018747	BC018747 Homo sapi
4	1147.2	85.9	1437	6	AR108865	AR108865 Sequence
5	1146.6	85.9	1630	9	BC024289	BC024289 Homo sapi
6	1145.8	85.8	1659	9	BC014667	BC014667 Homo sapi
7	1136	85.1	1430	6	AX149496	AX149496 Sequence
8	1133.8	84.9	7521	6	AX080951	AX080951 Sequence
9	1129.6	84.6	1353	6	AX277242	AX277242 Sequence
10	1127.6	84.5	1990	9	AK098817	AK098817 Homo sapi
11	1127.2	84.4	1419	12	AF019036	AF019036 Synthetic
12	1124.2	84.2	1401	9	AF027159	AF027159 Homo sapi
13	1123.4	84.1	1642	9	AK093806	AK093806 Homo sapi
14	1121.2	84.0	1673	9	HSIGG1LH	Y14737 Homo sapien
15	1120.2	83.9	1549	6	A21385	A21385 Plasmid DNA
16	1119.8	83.9	1624	9	HSIGG1KH	Y14735 Homo sapien
17	1119.6	83.9	1631	9	AK097010	AK097010 Homo sapi
18	1116.2	83.6	1666	9	BC006402	BC006402 Homo sapi
19	1111.6	83.3	1633	9	AK097367	AK097367 Homo sapi
20	1110.4	83.2	1633	9	AK097859	AK097859 Homo sapi
21	1109.6	83.1	3143	9	BC019046	BC019046 Homo sapi
22	1107	82.9	1637	9	AK093636	AK093636 Homo sapi
23	1104.8	82.8	1404	6	AX268679	AX268679 Sequence
24	1104.4	82.7	1639	9	AK097950	AK097950 Homo sapi
25	1103.2	82.6	1624	9	AK097206	AK097206 Homo sapi
26	1103	82.6	1620	9	AK097366	AK097366 Homo sapi
27	1102.2	82.6	2196	6	AX268709	AX268709 Sequence
28	1102.2	82.6	2226	6	AX268715	AX268715 Sequence
29	1100.4	82.4	1622	9	AK097359	AK097359 Homo sapi
30	1099.6	82.4	1627	9	AK097350	AK097350 Homo sapi
31	1097.8	82.2	1608	9	BC019337	BC019337 Homo sapi
32	1096.6	82.1	2190	6	AX268713	AX268713 Sequence
33	1096.6	82.1	2220	6	AX268719	AX268719 Sequence
34	1095.8	82.1	2193	6	AX268711	AX268711 Sequence
35	1095.8	82.1	2223	6	AX268717	AX268717 Sequence
36	1082.6	81.1	8120	6	AR116673	AR116673 Sequence
37	1082	81.0	4207	6	AX359930	AX359930 Sequence
38	1082	81.0	4207	6	AX382144	AX382144 Sequence
39	1082	81.0	5732	6	AX359932	AX359932 Sequence
40	1082	81.0	5732	6	AX382146	AX382146 Sequence
41	1082	81.0	9183	6	AX359933	AX359933 Sequence
42	1082	81.0	9183	6	AX382147	AX382147 Sequence
43	1072.6	80.3	1465	10	S79307	S79307 Ig gamma -1
44	1071.8	80.3	1605	9	BC025314	BC025314 Homo sapi
45	1071.2	80.2	1602	9	BC014258	BC014258 Homo sapi

ALIGNMENTS

RESULT 1
AX010615
LOCUS AX010615 1335 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 18 from Patent WO9958679.
ACCESSION AX010615
VERSION AX010615.1 GI:9997427
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.
TITLE Antibodies to cd23, derivatives thereof, and their therapeutic uses
JOURNAL Patent: WO 9958679-A 18 18-NOV-1999;
Bonnefoy JEAN YVES MARCEL PAUL (FR); Crowe SCOTT JAMES (GB); Rapson

Pred. No. is the number of results predicted by chance to have a

NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY (GB); SHEARIN JEAN (US)
Location/Qualifiers
1. .1335
/organism="synthetic construct"
/db.xref="taxon:32630"
/note="Humanised anti-CD23 antibody heavy chain variable region."
CDS
1. .1335
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAC07534.1"
/db.xref="GI:9997428"
/translation="EVQLVESGGGLVPGGSLRLCAASGFTFSGYWMSWRQAPGKGLWVAIRLTKVSSASTKPSVFPPLAPSSKTSSTGALGLVKDLPPEPVTWVSMNSGALTSQVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPRSCDKHTCPCPAPELAGAPSVFLPPKPKFLMSIRPTEVTCVVVDVSHEDPEKFNMYVDGVEVHNATKPREQINSYTRVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTTISKAGQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLVDSGGSEFLYSLKLVTDKSRWQGVNFSCSVMEALHNHYTQKSLSLSPGK"

BASE COUNT 321 a 414 c 360 g 240 t
ORIGIN

Query Match 100.0%; Score 1335; DB 6; Length 1335;
Best Local Similarity 100.0%; Pred. No. 2.4e-263;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGTGACGTGGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 60
DB 1 GAGGTGACGTGGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 60
QY 61 TCCTGTGCAGTACGCGATTCACTTTCAAGTGGCTACTGGATGTCCTCGGTCGCCAGGCT 120
DB 61 TCCTGTGCAGTACGCGATTCACTTTCAAGTGGCTACTGGATGTCCTCGGTCGCCAGGCT 120
QY 121 CCAGGGAAGGGCTCGAGTGGTGGTGAATTTAGATTGAAATCTGATTAATGCAACA 180
DB 121 CCAGGGAAGGGCTCGAGTGGTGGTGAATTTAGATTGAAATCTGATTAATGCAACA 180
QY 181 CATTATCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGA 240
DB 181 CATTATCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGA 240
QY 241 CTGTATCTCAATGACACACCTTGAAACCGGAGGACACAGCCGTGTTACTGTACAGAT 300
DB 241 CTGTATCTCAATGACACACCTTGAAACCGGAGGACACAGCCGTGTTACTGTACAGAT 300
QY 301 TTCATAGACTGGGGCCAGGAAACACTAGTACCGTCTCCTCAGCCTCCACRAGGCCCA 360
DB 301 TTCATAGACTGGGGCCAGGAAACACTAGTACCGTCTCCTCAGCCTCCACRAGGCCCA 360
QY 361 TCGGTCTTCCCTCGCACCTCTCCAAAGACACCTCTGGGGCCACAGCGCCCTGGGC 420
DB 361 TCGGTCTTCCCTCGCACCTCTCCAAAGACACCTCTGGGGCCACAGCGCCCTGGGC 420
QY 421 TGGCTGTGAAGGACTACTTCCCGAACCGGTGACGGTGTGCTGGAACTCAGCGCCCTG 480
DB 421 TGGCTGTGAAGGACTACTTCCCGAACCGGTGACGGTGTGCTGGAACTCAGCGCCCTG 480
QY 481 ACCAGGGGCTGCACACCTTCCCGGCTGCTCCTACAGTCTCAGGACTCTACTCCCTCAGC 540
DB 481 ACCAGGGGCTGCACACCTTCCCGGCTGCTCCTACAGTCTCAGGACTCTACTCCCTCAGC 540
QY 541 AGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT 600
DB 541 AGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT 600
QY 601 CACAAGCCAGCAACACCAAGGTGGACAGAAAGTGGAGGCCCAAAATCTTGTGACAAAAC 660
DB 601 CACAAGCCAGCAACACCAAGGTGGACAGAAAGTGGAGGCCCAAAATCTTGTGACAAAAC 660

QY 661 CACACATGCCACCGTGGCCAGCAGCTGAACCTCGGGGGGACACCTCAGTCTTCTCTTC 720
DB 661 CACACATGCCACCGTGGCCAGCAGCTGAACCTCGGGGGGACACCTCAGTCTTCTCTTC 720
QY 721 CCCCCAAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT 780
DB 721 CCCCCAAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGT 780
QY 781 GTGGAGCTGAGCCAGCAAGACCTTGAGGTCAAGTTCAACTGGTACGTGACGGCGTGAG 840
DB 781 GTGGAGCTGAGCCAGCAAGACCTTGAGGTCAAGTTCAACTGGTACGTGACGGCGTGAG 840
QY 841 GTGCATAATGCCAAAGCAAAAGCCGCGGGAGGAGCTACAAACAGCAGCTACCGTGTGTC 900
DB 841 GTGCATAATGCCAAAGCAAAAGCCGCGGGAGGAGCTACAAACAGCAGCTACCGTGTGTC 900
QY 901 AGCGTCTCTACCGTCTCTGACACAGGACTGGCTGAATGCAAGGAGTACAAGTGCAGGTC 960
DB 901 AGCGTCTCTACCGTCTCTGACACAGGACTGGCTGAATGCAAGGAGTACAAGTGCAGGTC 960
QY 961 TCCAAACAAAGCCCTCCAGCCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCC 1020
DB 961 TCCAAACAAAGCCCTCCAGCCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCC 1020
QY 1021 CGAAGAACACAGGTGTACACCTGCCCTCCCGGATGAGCTGACCAAGAACAGGTC 1080
DB 1021 CGAAGAACACAGGTGTACACCTGCCCTCCCGGATGAGCTGACCAAGAACAGGTC 1080
QY 1081 AGCCTGACCTGCTGGTCAAGGCTTCTATCCACCGACATCGCGTGGAGTGGAGAGC 1140
DB 1081 AGCCTGACCTGCTGGTCAAGGCTTCTATCCACCGACATCGCGTGGAGTGGAGAGC 1140
QY 1141 AATGGGACCGCGGAGAAACACTACAAGACACCGCTCCCGTCTGGACTCCGACGGCTCC 1200
DB 1141 AATGGGACCGCGGAGAAACACTACAAGACACCGCTCCCGTCTGGACTCCGACGGCTCC 1200
QY 1201 TTCCTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGAGGGAAGCTCTTC 1260
DB 1201 TTCCTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGAGGGAAGCTCTTC 1260
QY 1261 TCATGCTCCGTGATCATGAGGCTCTGCACACCACTACACGAGAGGCTCTCCCTG 1320
DB 1261 TCATGCTCCGTGATCATGAGGCTCTGCACACCACTACACGAGAGGCTCTCCCTG 1320
QY 1321 TCTCCGGTAAATGA 1335
DB 1321 TCTCCGGTAAATGA 1335

RESULT 2
AX010646/c
LOCUS AX010646 1335 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 49 from Patent WO9958679.
ACCESSION AX010646
VERSION AX010646.1 GI:9997455
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Bonnefoy,J.Y., Crowe,S.J., Rapson,N.T., Ellis,J.H. and Shearin,J.
TITLE Antibodies to cd23, derivatives thereof, and their therapeutic uses
JOURNAL Patent: WO 9958679-A 49 18-NOV-1999;
Bonnefoy JEAN YVES MARCEL PAUL (FR); CROWE SCOTT JAMES (GB); RAPSON NICHOLAS TIMOTHY (GB); GLAXO GROUP LTD (GB); ELLIS JONATHAN HENRY (GB); SHEARIN JEAN (US)

FEATURES
source location/Qualifiers
1. .1335
/organism="synthetic construct"
/db.xref="taxon:32630"
/note="Humanised anti-CD23 antibody heavy chain variable region"
BASE COUNT 240 a 360 c 414 g 321 t

ORIGIN

Query Match 100.0%; Score 1335; DB 6; Length 1335;
Best Local Similarity 100.0%; P-Value 2.4e-263; Mismatches 0; Indels 0; Gaps 0;
Matches 1335; Conservative 0;

QY 1 GAGGTGACGCTGGTGGAGCTTGGTAAAGCCGGGGGTCCTTACAGCTC 60
DB 1335 GAGTCCAGCTGGTGGAGCTTGGTAAAGCCGGGGGTCCTTACAGCTC 1276
QY 61 TCTGTGACGCTAGCGGATTCACCTTTACAGTGGCTACTGGATGCTCCGGTCCGCCAGGCT 120
DB 1275 TCTGTGACGCTAGCGGATTCACCTTTACAGTGGCTACTGGATGCTCCGGTCCGCCAGGCT 1216
QY 121 CCAGGGAAGGGCTCCAGTGGGTGCTGAATTTAGATTCAAATTCGATAATTCACACA 180
DB 1215 CCAGGGAAGGGCTCCAGTGGGTGCTGAATTTAGATTCAAATTCGATAATTCACACA 1156
QY 181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
DB 1155 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 1096
QY 241 CTGTATCTGCAATGAACAGCTGAAACCGGAGGACACAGCGGTGTATTTACTGTACAGAT 300
DB 1095 CTGTATCTGCAATGAACAGCTGAAACCGGAGGACACAGCGGTGTATTTACTGTACAGAT 1036
QY 301 TTCATAGACTGGGGCCAGGGAACACTAGTCACCGTCTCTCAGCTTCCACCAAGGGGCCA 360
DB 1035 TTCATAGACTGGGGCCAGGGAACACTAGTCACCGTCTCTCAGCTTCCACCAAGGGGCCA 976
QY 361 TCGGTCTTCCCTTCCGACCCCTCTCTCAAGAGACACTCTGGGGGACAGCGCCCTGGGC 420
DB 975 TCGGTCTTCCCTTCCGACCCCTCTCTCAAGAGACACTCTGGGGGACAGCGCCCTGGGC 916
QY 421 TGCTGTGTCAGAGCTACTTCCCGAACCGGTGACGGTGTCTGAGACTCAGCGCCCTG 480
DB 915 TGCTGTGTCAGAGCTACTTCCCGAACCGGTGACGGTGTCTGAGACTCAGCGCCCTG 856
QY 481 ACCAGCGGGCTGCACACCTTCCCGGCTCTCTACAGTCTCTCAGGACTTACTTCCCTCAGC 540
DB 855 ACCAGCGGGCTGCACACCTTCCCGGCTCTCTACAGTCTCTCAGGACTTACTTCCCTCAGC 796
QY 541 AGCGTGTGACCGTCCGCTCCAGAGCTTGGGACCCAGCTTACATCTGCAACGCTGAAT 600
DB 795 AGCGTGTGACCGTCCGCTCCAGAGCTTGGGACCCAGCTTACATCTGCAACGCTGAAT 736
QY 601 CACAAGCCAGCACACAGGTTGGACAAAGTTGGAGCCCAAAATCTTGTGACAAAAT 660
DB 735 CACAAGCCAGCACACAGGTTGGAGCAAGAAAGTTGGAGCCCAAAATCTTGTGACAAAAT 676
QY 661 CACACATGCCCGCTGCCAGCACCTGAACTCCGGGGGACCGCTCAGTCTTCTCTCTTC 720
DB 675 CACACATGCCCGCTGCCAGCACCTGAACTCCGGGGGACCGCTCAGTCTTCTCTCTTC 616
QY 721 CCCCCAAAACCCAGGACACCTCTATGATCTCCCGGACCCCTGAGTGCATCGTGGTGG 780
DB 615 CCCCCAAAACCCAGGACACCTCTATGATCTCCCGGACCCCTGAGTGCATCGTGGTGG 556
QY 781 GTGAGCTGAGCCAGGACACCTGAGTCAAGTCAAGTGTACCTGGTGGACCGCTGGAG 840
DB 555 GTGAGCTGAGCCAGGACACCTGAGTCAAGTCAAGTGTACCTGGTGGACCGCTGGAG 496
QY 841 GTGCATATGCCAAGACAAAACCGGGAGGAGCAGTACAAACAGCAGCTACCGTGGTGG 900
DB 495 GTGCATATGCCAAGACAAAACCGGGAGGAGCAGTACAAACAGCAGCTACCGTGGTGG 436
QY 901 AGCGTCTCAGCGTCTCCAGGAGCTGCTGAATGGCAAGGAGTACAAGTGCAGAGGTC 960
DB 435 AGCGTCTCAGCGTCTCCAGGAGCTGCTGAATGGCAAGGAGTACAAGTGCAGAGGTC 376
QY 961 TCCAAAGAGCCCTCCAGCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGGAGCC 1020
DB 375 TCCAAAGAGCCCTCCAGCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGGAGCC 316

QY 1021 CGAAGACACAGGTGTACACCTGCCCTCCCGGATGAGCTGACCAAGAACAGGTC 1080
DB 315 CGAAGACACAGGTGTACACCTGCCCTCCCGGATGAGCTGACCAAGAACAGGTC 256
QY 1081 AGCTGTACCTCCCTGGTCAAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGC 1140
DB 255 AGCTGTACCTCCCTGGTCAAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGC 196
QY 1141 AATGGGACCGGAGAGACAACTACAAGACACGCTCCCGTGGTGGAGTCCGAGCGGTCC 1200
DB 195 AATGGGACCGGAGAGACAACTACAAGACACGCTCCCGTGGTGGAGTCCGAGCGGTCC 136
QY 1201 TTTCTTCTCTACAGCAAGCTCACGCTGACAAAGAGCAGGTGGGAGGGAAGCTCTTC 1260
DB 135 TTTCTTCTCTACAGCAAGCTCACGCTGACAAAGAGCAGGTGGGAGGGAAGCTCTTC 76
QY 1261 TCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACAGCAGAGAGGCTTCCCTG 1320
DB 75 TCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACAGCAGAGAGGCTTCCCTG 16
QY 1321 TCTCCGGGTAATGA 1335
DB 15 TCTCCGGGTAATGA 1

RESULT 3
BC018747
LOCUS BC018747 1679 bp mRNA linear PRI 11-DEC-2001
DEFINITION Homo sapiens, Similar to immunoglobulin heavy constant gamma 3 (G3m marker), clone MGC:31937 IMAGE:4851063, mRNA, complete cds.
ACCESSION BC018747
VERSION BC018747.1 GI:17511791
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1679)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 40 Row: 1 Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction, Similarity but not identity to protein.
Location/Qualifiers
1..1679
/organism="Homo sapiens"

FEATURES
source

```

/db_xref="taxon:9606"
/clones="MGC:31937 IMAGE:4851063"
/tissue_type="Primary B-Cells from Tonsils"
/clone_lib="NIH_MGC_48"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
63.11475

```

CDS

/product="Similar to immunoglobulin heavy constant gamma 3
 (G3m marker)"
 /protein_id="AAH18747.1"
 /db_xref="GI:17511792"
 /translation="MELGSLWFLVAILEGVCQEVQLVSGCGILVQPGGSLRLSCVVS
 GFTFSIMSWVRQAPGKLEWVAMIKDGEKYYVDVSGKRTISDNAKNSLYLQM
 NSLAAGCLVYDYFCARDGSSYRDWDPDNGQGLTVASASTKGPSPFLAPSSKSGT
 TGAALGCLVYDYFPFPTVSMNGSLTSGVHTFPAVLQSGLYSLSSWVTPVSSGLG
 QTVICNVNHKPSNTVDKKVEPKCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMV
 SRTPETVCTVVDVSEDDPEVKNTVDGVSEVHNKATPQREQYNSYTRVYVSIVLVHLQ
 DWLNGEKCKYVSWSKALPAPEKTIISKAGQGPQEPVYTPPSRDELTKQVSLSLG
 GPKPSDIAVQWESNGQSPENNYKTPTPVLDSDGSGFFLYSLKTVDSKRWQOQNGVFCSG
 MHEALINHYTQKSLSLPEK"

430 a	506 c	452 q	291 t
-------	-------	-------	-------

ORIGIN

Query Match 86.6%; Score 1156; DB 9; Length 1679;
Best Local Similarity 92.1%; Pred. No. 1.1e-226;
Matches 1254; Conservative 0; Mismatches 75; Indels 33

60	1	GAGTGTGAGCTGTGGAGTCTGGGGGAGCGTTGGTAAAGCCCGGGGGTCCCTTAGACTC	60
QY			
120	120	GAGTGTGAGCTGTGGAGTCTGGGGGAGCGTTGGTCAAGCTGGGGGTCCCTGAGACTC	120
DB			
179	61	TCCTGTGAGCTAGCGGATTCACCTTTCAGTGGCTACTGATGTCTCTGGTCCGCGAGGCT	120
QY			
239	180	TCCTGTGTAGTCTCTGGATTCACCTTTAGTAGTTATTGGATGAGCTGGTCCGCGAGGCT	180
DB			
296	121	CCAGGGAAGGGCTCGAGTGGTGTGAAATAGATTGAAATCTGATAATATTGCAACA	180
QY			
354	240	CCAGGGAAGGGCTGGAGTGGGTGGCCACA-----TAAAGCAAGATTGGAAGTGAAGA	293
DB			
413	181	CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTGA	240
QY			
473	294	TACTATGTGAGCTCTGTGAAGGCCGANTTCACATCTCCAGAGACACGCCAAGACTCA	353
DB			
496	241	CTGTATCTGCAATGAACAGCCTGAAACCGAGGACACAGCCGTGATATTACTGTAC----	296
QY			
534	354	CTGTATCTGCAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGA	413
DB			
593	297	-----AGATTTTCATAGACTGGGGCCAGGGACACTAGTCACC	333
QY			
613	414	GATGCGACGAGCTGGTACAGGGACTGGTTTCGACCCCTGGGCGCAGGAAACCCCTGGTCACC	473
DB			
634	334	GTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGACACCTCCTCTCCAGAGC	393
QY			
693	474	GTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGACACCTCCTCCAGAGC	533
DB			
713	394	ACCTTGGGGGCACAGCGGCCCTGGGCTGCCTGTGAAGGACTACTTCCCGAACCGGTG	453
QY			
733	534	ACCTTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCGAACCGGTG	593
DB			
753	454	ACGGTGTGCTGGAATCAGCGGCCCTGACCAGGGCGTGCACACTTCCCGGCTGTCCCTA	513
QY			
773	594	ACGGTGTGCTGGAATCAGCGGCCCTGACCAGGGCGTGCACACTTCCCGGCTGTCCCTA	653
DB			
793	514	CAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGC	573
QY			
813	654	CAGTCCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGC	713
DB			
833	574	ACCCAGACTACATCTCGACGTTGAATCAGACGCCACCAACACAGGTTGGACAGAA	633
QY			
853	714	ACCCAGACTACATCTCGACGTTGAATCAGACGCCACCAACACAGGTTGGACAGAA	773
DB			
873	634	GTGGAGCCCAATCTGTGTGACAAATCTACACATGCCACCGTGCACGACCTGAATC	693
QY			

[illegible]

RESULT_4				PAT 14-FEB-2001
LOCUS	ARI08865		DNA	linear
DEFINITION	Sequence 7 from patent US 6113898.	1437 bp		
ACCESSION	ARI08865			
VERSION	ARI08865.1 GI:12825141			
KEYWORDS	.			
SOURCE	Unknown..			
ORGANISM	Unknown.			
REFERENCE	Unclassified 1 (bases 1 to 1437)			
AUTHORS	Anderson,D.R., Brans,P., Hanna,N., Shestowsky,W.S. and Heard,C. Human B7.1-specific primatized antibodies and transfectomas expressing said antibodies			
TITLE	Patent: US 6113898-A 7 05-SEP-2000; Location/Qualifiers 1..1437 ./organism='unknown'			
JOURNAL				
FEATURES	source			
BASE COUNT	329 a	451 c	387 g	270 t
ORIGIN				

Query Match 85.9%; Score 1147.2; DB 6; Length 1437;
 Best Local Similarity 90.7%; Pred. No. 7e-225;
 Matches 1252; Conservative 0; Mismatches 83; Indels 45; Gaps 1;

1:


```
/codon_start=1
/product="Unknown (protein for MGC:39273)"
/protein_id="AAH24289.1"
/db_xref="GI:18999465"
/translation="MELGLRWFLVAILEGVCEVQLVESGGLVKPGSLRLSCAAS
GTFYSYNNWRQAPKGLKLEWVSMSSSSIIYADSVKGRFTISRDNKNSLYLQM
NSLRABDTAVYICARDLRLTYSYFDLWGRFTLVSSASTKGLSPVPLAPSSKSTL
GSLAALGCVLYKDFPFPVTVSNWGSALTSGVTFPAVLQSSGLVSLSSVTVPSSSLG
TOTYICNVNHNKPSNTKDKKVPKSCDKTHTPCPGAPPELLGLGSPVFPKPKDITLM
ISRTPEVTCCVVVDVSHEDPEVKFNVDGVVHNKTRPREOYNSTVRYVSVLTVLH
OWPLNGKEYKCVSKNKPALPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCL
VFYFPPSDHYAVESWNGQPENNYKTPPPVLDSDGEFFLYSKLTVDKSRWQQGNVFSCS
VMHEALHNHYTQKSLSLSPGK"
BASE COUNT      374 a      518 c      442 g      296 t
ORIGIN

Query Match      85.9%; Score 1146.6; DB 9; Length 1630;
Best Local Similarity 91.8%; Pred. No. 9.2e-225; Mismatches 79; Indels 36; Gaps 2;
Matches 1250; Conservative 0;

QY  1  GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
      |||
DB 121 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTCAAGCCTGGGGGGTCCCTGAGACTC 180
      |||

QY  61 TCCTGTGCAGCTAGCAGTACTTTCAGTGGCTACTGGGATGTCCTGGGTCCGCCAGGCT 120
      |||
DB 181 TCCTGTGCAGCTAGCAGTACTTTCAGTGGCTACTGGGATGTCCTGGGTCCGCCAGGCT 240
      |||

QY 121 CCAGGGAAGGGGCTCGAGTGGGTGCTGAAATTAAGATTGAATCTGATATTAATGCAACA 180
      |||
DB 241 CCAGGGAAGGGGCTCGAGTGGGTGCTGATCA-----TGAGTAGTAGTAGTACATACATA 294
      |||

QY 181 CATTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
      |||
DB 295 TACTATCAGCACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACACACGCAAGAATCA 354
      |||

QY 241 CTGTATCTGCAAAATGAACAGCTTGAACAGGAGACACAGCGGTGATTACTGTAC---- 296
      |||
DB 355 CTGTATCTGCAAAATGAACAGCTGAGAGCGGAGGACACAGCGCTGTGATTACTGTGGAGA 414
      |||

QY 297 -----AGATTTCATAGACTGGGGCCAGGGAACACTAGTC 330
      |||
DB 415 GATCTCGCCAGCTAACTTCTACTGTGACTTGCATCTCTGGGGCCGTGGCACCCCTGGTC 474
      |||

QY 331 ACCGTCTCTCAGCTCCACCAAGGGCCATCGTCTTCCCTCGCTGSCACCCCTCTCCAAG 390
      |||
DB 475 ACTGTCTCTCAGCTCCACCAAGGGCCATCGTCTTCCCTCGCTGSCACCCCTCTCCAAG 534
      |||

QY 391 AGCACTCTGGGGGCACAGCGGCCCTGGGCTGCTGCTCAAGACTACTTCCCGCGAACC 450
      |||
DB 535 AGCACTCTGGGGGCACAGCGGCCCTGGGCTGCTGCTCAAGACTACTTCCCGCGAACC 594
      |||

QY 451 GTGACGCTGTGCTGGAATCAGGCGCCCTGACCAAGCGGCGTGACACACTTCCCGGCTGTC 510
      |||
DB 595 GTGACGCTGTGCTGGAATCAGGCGCCCTGACCAAGCGGCGTGACACACTTCCCGGCTGTC 654
      |||

QY 511 CTACAGTCTCAGACTCTACTCCTCAGCAGCGTGTGTACCGTGGCTCCACAGCGCTTG 570
      |||
DB 655 CTACAGTCTCAGACTCTACTCCTCAGCAGCGTGTGTACCGTGGCTCCACAGCGCTTG 714
      |||

QY 571 GGCACCCAGACTCATCTCTGAAGCTGAATCACAAGCCCGAGCAACACCAAGGTGGACAAG 630
      |||
DB 715 GGCACCCAGACTCATCTCTGAAGCTGAATCACAAGCCCGAGCAACACCAAGGTGGACAAG 774
      |||

QY 631 AAGTGGAGCCCAATCTTGTGACAAAACCTACACATGCCACCGTCCCGCAGCACCTGAA 690
      |||
DB 775 AAGTGGAGCCCAATCTTGTGACAAAACCTACACATGCCACCGTCCCGCAGCACCTGAA 834
      |||

QY 691 CTCGGGGGGGACCGCTCAGTCTTCTCTTCCGCCCAAAACCCAGGACACCCCTCATGATC 750
      |||
DB 835 CTCCTGGGGGACCGCTCAGTCTTCTCTTCCGCCCAAAACCCAGGACACCCCTCATGATC 894
      |||

QY 751 TCCCGGACCCCTGAGGTCACATGCGTGGTGTGAGCGCTGAGCCACGAAGACCCCTGAGGTC 810
      |||
```

```
Db 895 TCCCGGACCCCTGAGTGCACATGCGTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTC 954
      |||
QY 811 AAGTTCAACTGGTACGTGGAGCGCGTGGAGGTGCATAATGCCAAGACAAAGACCCCGGGAG 870
      |||
DB 955 AAGTTCAACTGGTACGTGGAGCGCGTGGAGGTGCATAATGCCAAGACAAAGACCCCGGGAG 1014
      |||

QY 871 GAGCAGTACAACAGACAGTACCGTGGTGCAGCGGCTCTCACCCTGCTGCACAGACTGG 930
      |||
DB 1015 GAGCAGTACAACAGACAGTACCGTGGTGCAGCGGCTCTCACCCTGCTGCACAGACTGG 1074
      |||

QY 931 CTGAATGCCAAGGAGTACAAGTGCAGGTCTCCAAACAAGCCCTCCCAAGCCCATCGAG 990
      |||
DB 1075 CTGAATGCCAAGGAGTACAAGTGCAGGTCTCCAAACAAGCCCTCCCAAGCCCATCGAG 1134
      |||

QY 991 AAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACACACAGGTGTACACCTCGCCCCCA 1050
      |||
DB 1135 AAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACACACAGGTGTACACCTCGCCCCCA 1194
      |||

QY 1051 TCCCGGGATGAGCTGACCAAGAACCCAGGTTCAGCTGACCTGCCTGGTCAAAAGGCTTCTAT 1110
      |||
DB 1195 TCCCGGGATGAGCTGACCAAGAACCCAGGTTCAGCTGACCTGCCTGGTCAAAAGGCTTCTAT 1254
      |||

QY 1111 CCCAGCGACATCGCGTGGAGTGGGAGCAATGGCAGCGGAGAACAACTACAAGACC 1170
      |||
DB 1255 CCCAGCGACATCGCGTGGAGTGGGAGCAATGGCAGCGGAGAACAACTACAAGACC 1314
      |||

QY 1171 AGCGCTCCCGTCTGGACTCCGACGGCTCTTCTTCTTACAGCAAGCTCACCGTGGAC 1230
      |||
DB 1315 AGCGCTCCCGTCTGGACTCCGACGGCTCTTCTTCTTACAGCAAGCTCACCGTGGAC 1374
      |||

QY 1231 AGAGCAGGTGGCAGCGGGAACGCTTCTCATGCTCCGTCGTCATGATGAGGCTCTGCAC 1290
      |||
DB 1375 AGAGCAGGTGGCAGCGGGAACGCTTCTCATGCTCCGTCGTCATGATGAGGCTCTGCAC 1434
      |||

QY 1291 AACCCTACACGACGAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1335
      |||
DB 1435 AACCCTACACGACGAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1479
      |||

RESULT 6
BC014667      1659 bp      mRNA      linear      PRI 26-SEP-2001
LOCUS      Homo sapiens, Similar to immunoglobulin heavy constant gamma 3 (G3m
DEFINITION      marker), clone MGC:23153 IMAGE:4850078, mRNA, complete cds.
ACCESSION      BC014667
VERSION      BC014667.1 GI:15779221
KEYWORDS      MGC.
SOURCE      Homo sapiens.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1659)
AUTHORS      Strausberg,R.
TITLE      Direct Submission
JOURNAL      Submitted (24-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT      Contact: MGC help desk
Email: cgapbs-re@mail.nih.gov
Tissue procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
```

Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott zuiderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 34 Row: A Column: 20.
Location/Qualifiers

FEATURES

source

1. 1659
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:23153 IMAGE:4850078"
/tissue_type="Spleen"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
69. 1508

CDS

/codon_start=1
/product="Similar to immunoglobulin heavy constant gamma 3 (G3m marker)"
/protein_id="AAH14667.1"
/db_xref="GI:15779222"
/translation="MKPGLSKWLPALKGVCEVOLVESGGGLVKAGSLRLSCAAS GFSPSDAMSWAQPPKPGKLEWLRKRSDDGETTEAHHVKGKFIISRDDSKIMYIM QMSLKTEDTAVYICNDARKSVLSLEPNYYHGMNVWEGTIVTSASATKSPVPL APSKTSSTGTAALCLVKDYFPPEPTVSNWGSALTSGVHTFPFPAVLSGLYSLSSV TVPSSISGTQTYICNVNHPKSNKVKKKVPKSDKTHTPCPAPPELLGGLSVFLFP PKPKDTLMIISRTPEVTVCVVVDVSHEDPEVKENYVDGVEVHNNAKTPREOYNSTYRV VSVLTLDHQLNGKEYKCKVSNKALPAPIEKILSKAKGQPREPQVYITLPPSRDELTK NOVSLTCLKGFPSDIAVEWESNGPENNYKTPPVLVSDSGSFFLYSLKLTVDKSRWQ QGNVFSVNHREALHNHYTKLSLSLSPG"
BASE COUNT 397 a 505 c 457 g 300 t
ORIGIN

Query Match 85.8%; Score 1145.8; DB 9; Length 1659;
Best Local Similarity 90.6%; Pred. No. 1.3e-224;
Matches 1253; Conservative 0; Mismatches 82; Indels 48; Gaps 1;

QY 1 GAGGTGACGTGGTGGAGTCTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTC 60
DB 126 GAGGTGACGTGGTGGAGTCTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTC 185
QY 61 TCCTGTGACGTAGCGGATTCACHTTTCAGTGGCTACTGGATGTCCTGGTCCGCCAGCT 120
DB 186 TCCTGTGACGCTCTGGATTCAGTTTCAGTGGCTGATGCTGGTGGTCCGCCAGCT 245
QY 121 CCAGGGAAGGGCTCGAGTGGTCTCGAAATTAGATTGAAATCTGATAATTATGCAACA 180
DB 246 CCAGGGAAGGGCTCGAGTGGTCTGGCCGCAATTAAGGAAGAAAGATGTTGGGACACACA 305
QY 181 CATTATGCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
DB 306 GAGTACGCTGCACAGCTGAAAGGAGAGATTCATCTCTAGAGACGACTCAAAATACATG 365
QY 241 CTGTATCTGCAATGAACAGCTGAAACCCAGGACACAGCCGTGATTACTGTA----- 295
DB 366 GTGTATATGCAGATGAACAGTCTGAAGACCGAGGACAGCCGCTATTACTGTAATACA 425
QY 296 -----CAGATTTTCATAGACTGG 312
DB 426 GATGCCCTCAGTAGGATCTTGGAGTGGCCCAATTAATTATCAGCGGTATGAACGTCTGG 485
QY 313 GCCCAGGGAACACTAGTACCGCTCTCTCTCAGCTCCACCAAGGGCCCATCGTCTTCCCC 372
DB 486 GGTGAAGGACACACGCTCACCCTCTCTTACGCTCCACCAAGGGCCCATCGTCTTCCCC 545
QY 373 CTGGCACCTCTCTCAAGAGCACCTCTCTGGGGACAGGGCCCTGGGCTGGCTGGTCAAG 432
DB 546 CTGGCACCTCTCTCAAGAGCACCTCTCTGGGGACAGGGCCCTGGGCTGGCTGGTCAAG 605
QY 433 GACTACTTCCCGGAACCGGTGACGGTGTCTGGGAACCTACAGCGCCCTCACCAGCGCGTG 492
DB 606 GACTACTTCCCGGAACCGGTGACGGTGTCTGGGAACCTACAGCGCCCTCACCAGCGCGTG 665

QY 493 CACACCTTCCCGCTGTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACC 552
DB 566 CACACCTTCCCGCTGTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACC 725
QY 553 GTCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAGCCACG 612
DB 726 GTCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAGCCACG 785
QY 613 AACACCAAGTGGACAGAAGTGGAGCCCAAAATCTTGTGACAAAACCTACACATGCCCA 672
DB 786 AACACCAAGTGGACAGAAGTGGAGCCCAAAATCTTGTGACAAAACCTACACATGCCCA 845
QY 673 CCCTGCCACGACCTGAACCTCGCGGGGACCGCTCAGTCTTCTCTTCCCCCCCCAAACCC 732
DB 846 CCCTGCCACGACCTGAACCTCTCGGGGACCGCTCAGTCTTCTCTTCCCCCCCCAAACCC 905
QY 733 AAGACACCTCATATGATCTCCCGGACCCCTGAGGTACATGTGCTGTGGTGGACGTGAGC 792
DB 906 AAGACACCTCATATGATCTCCCGGACCCCTGAGGTACATGTGCTGTGGTGGACGTGAGC 965
QY 793 CACGAAGACCTCAGGTCAAGTTCAACTGGTAGTGGAGCGGTGGAGTGGATATGCC 852
DB 966 CACGAAGACCTCAGGTCAAGTTCAACTGGTAGTGGAGCGGTGGAGTGGATATGCC 1025
QY 853 AAGACAAAGCGCGGGAGGAGCAGTACAACAGCACCTACCGTGTGTGCTCAGCGTCCCTCAC 912
DB 1026 AAGACAAAGCGCGGGAGGAGCAGTACAACAGCACCTACCGTGTGTGCTCAGCGTCCCTCAC 1085
QY 913 GTCTGTACACGAGTGGCTGAATGGCAGGAGTACAAGTGAAGTGTCTCCAAACAAGCC 972
DB 1086 GTCTGTACACGAGTGGCTGAATGGCAGGAGTACAAGTGTCTCCAAACAAGCC 1145
QY 973 CTCCAGCCCTCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAG 1032
DB 1146 CTCCAGCCCTCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAG 1205
QY 1033 GTGTACACCTTGGCCCTCATCCCGGATGAGTCAACCAAGAACAGTCAAGCTGACCTGC 1092
DB 1206 GTGTACACCTTGGCCCTCATCCCGGATGAGTCAACCAAGAACAGTCAAGCTGACCTGC 1265
QY 1093 CTGGTCAAGGCTTCTATCCACGACATGCGCGTGGAGTGGAGGAGCAATGGGACGCG 1152
DB 1266 CTGGTCAAGGCTTCTATCCAGCAGATGCGCGTGGAGTGGAGGAGCAATGGGACGCG 1325
QY 1153 GAGAAACATACAGACACCGCTCGCGTGTGAGTCCGACGGCTCTTCTCTCTCTAC 1212
DB 1326 GAGAAACATACAGACACCGCTCGCGTGTGAGTCCGACGGCTCTTCTCTCTCTAC 1385
QY 1213 AGCAAGTCAAGTGGACAGAGAGTGGCAGGAGGAGCAAGCTTCTCTATGCTCCGTG 1272
DB 1386 AGCAAGTCAAGTGGACAGAGAGTGGCAGGAGGAGCAAGCTTCTCTATGCTCCGTG 1445
QY 1273 ATGATGAGGCTCTGACACACCACTACACGACAGAGGCTCTCCCTGTCTCGGGTAA 1332
DB 1446 ATGATGAGGCTCTGACACACCACTACACGACAGAGGCTCTCCCTGTCTCGGGTAA 1505
QY 1333 TGA 1335
DB 1506 TGA 1508

RESULT 7

AX419496
LOCUS AX419496 1430 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 1 from Patent WO0188132.
ACCESSION AX419496
VERSION AX419496.1 GI:21523919
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Hooper,D.C. and Dietzschold,B.
TITLE Rabies virus-specific neutralizing human monoclonal antibodies and
nucleic acids and related methods
JOURNAL Patent: WO 0186132-A 1 22-NOV-2001;
Thomas Jefferson University (US)
FEATURES Location/Qualifiers
source 1..1430
/organism="Homo sapiens"
BASE COUNT 326 a 438 c 396 g 270 t
ORIGIN /db_xref="taxon:9606"
Query Match 85.1%; Score 1136; DB 6; Length 1430;
Best Local Similarity 90.3%; Pred. No. 1.4e-222;
Matches 1249; Conservative 0; Mismatches 80; Indels 45; Gaps 2;
QY 1 GAGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
DB 61 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCCTTGAGACTC 120
QY 61 TCCTGTGCAGCTACGCGATTTCATTTTCAGTGGCTACTTGGATGTCCTGGGTCCGCCAGGCT 120
DB 121 TCCTGTGCAGCTCTGATTTCACCTTTAGCACTATGCCATGAGCTGGGTCCGCCAGGCT 180
QY 121 CCAGGGAAGGGGTCGAGTGGGTGGTGGAAATAGATTGAAATCTGATTAATGCAACA 180
DB 181 CCAGGGAAGGGGTCGAGTGGGTGGTGGAAATAGATTGAAATCTGATTAATGCAACA 234
QY 181 CATTATCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGA 240
DB 235 TATTGGCAGACTCCGTGAAGGCCGGTTCACCATCTCCAGAGCAATTCACCAAGACAG 294
QY 241 CTGTATCTGCAATGAACAGCTGAAACCGAGGACACAGCCGTGATTACTGTAC - - - - 296
DB 295 CTGTATCTGCAATGAACAGCTGAGAGCGGAGGACACAGCCGTGATTACTGTGCGAAA 354
QY 297 - - - - -AGATTTCAATAGACTGGGGCCAGGGA 321
DB 355 GATCGAGAGGTTACTATGATAGTTGTACTTAAATGGAGGCTTTTGACTACTGGGGCCAGGGA 414
QY 322 ACCTAGTACCGGTCTCTCAGCCTCCACCAAGGCCCATCGCTGTCCCTCGGACCC 381
DB 415 ACCGGGTACCGGTCTCTCCGGCTCCACCAAGGGCCATCGGTCTTCCCTTGGCACCC 474
QY 382 TCCTCCAAAGACACCTCTCTGGGGCACAGCGGCCCTGGGTCTGGTCAAGGACTACTTC 441
DB 475 TCCTCCAAAGACACCTCTGGGGCACAGCGGCCCTGGGTCTGGTCAAGGACTACTTC 534
QY 442 CCGAACCCTGAGGTGTCTGGAACTCAGGCGCCCTGACCAAGCGGTGCAACCTTC 501
DB 535 CCGAACCCTGAGGTGTCTGGAACTCAGGCGCCCTGACCAAGCGGTGCAACCTTC 594
QY 502 CCGCTCTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCC 561
DB 595 CCGCTCTCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCC 654
QY 562 AGCAGCTTGGGACCCAGACCTATCTGCAAGCTGAATCACAAGCCCAAGGACACCAAG 621
DB 655 AGCAGCTTGGGACCCAGACCTATCTGCAAGCTGAATCACAAGCCCAAGGACACCAAG 714
QY 622 GTGGACAAGAAAGTGGAGCCCAATCTTGTGACAAAACCTACACATGCCACCGTCCCA 681
DB 715 GTGGACAAGAAAGTGGAGCCCAATCTTGTGACAAAACCTACACATGCCACCGTCCCA 774
QY 682 GCACCTGAACCTCGGGGGACCGTCTAGTCTTCTTCCCTCCCAAAACCCCAAGGACAC 741
DB 775 GCACCTGAACCTCGGGGGACCGTCTAGTCTTCTTCCCTCCCAAAACCCCAAGGACAC 834
QY 742 CTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGTGGTGGTGGTGGTGGT 801
DB 835 CTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 894

QY 802 CCTGAGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATATATGCAAGACAAG 861
DB 895 CCTGAGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATATATGCAAGACAAG 954
QY 862 CGCGGGGAGGACGAGTACAACAGCAGCTACCGTGTGGTTCAGGCTCCTCAGCTCCTGCAC 921
DB 955 CGCGGGGAGGACGAGTACAACAGCAGCTACCGTGTGGTTCAGGCTCCTCAGCTCCTGCAC 1014
QY 922 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGAGTCTCCAAACAAAGCCCTCCAGCC 981
DB 1015 CAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGAGTCTCCAAACAAAGCCCTCCAGCC 1074
QY 982 CCATCGAAGAAACCATCTCCAAAGCCAAAGGAGCGAGCCCGGAGAACACAGGTGTACAC 1041
DB 1075 CCATCGAAGAAACCATCTCCAAAGCCAAAGGAGCGAGCCCGGAGAACACAGGTGTACAC 1134
QY 1042 CTGCCCCCATCCGGATGAGCTGACCAAGAACACAGCTCAGCCTGACCTGGTCAAA 1101
DB 1135 CTGCCCCCATCCGGGAGGAGTACCAAGAACACAGCTCAGCCTGACCTGGTCAAA 1194
QY 1102 GGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGCAATGGCGAGCGGAGAACAC 1161
DB 1195 GGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGCAATGGCGAGCGGAGAACAC 1254
QY 1162 TACAAGACACCGCTCCCGTGGTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTC 1221
DB 1255 TACAAGACACCGCTCCCGTGGTGGACTCCGACGGCTCCTTCTTCTCTATATGCAAGCTC 1314
QY 1222 ACCGTGGACAGAGCAGGTGGCAGCGGAGAACGCTTCTCATGCTCGGTGATGATGAG 1281
DB 1315 ACCGTGGACAGAGCAGGTGGCAGCGGAGAACGCTTCTCATGCTCGGTGATGATGAG 1374
QY 1282 GCTCTGCACACCACTACACGAGAACGCTCTCCCTGTCTCCGGGTAATGA 1335
DB 1375 GCTCTGCACACCACTACACGAGAACGCTCTCCCTGTCTCCGGGTAATGA 1428

RESULT 8
AX080951
LOCUS AX080951 7521 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 1 from Patent WO0109303.
ACCESSION AX080951
VERSION AX080951.1 GI:13169888
KEYWORDS synthetic construct.
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 7521)
AUTHORS Hermanson,G.G.
TITLE Flt-3 ligand-encoding polynucleotide as a polynucleotide-based
vaccine enhancer
JOURNAL Patent: WO 0109303-A 1 08-FEB-2001;
VICAL INCORPORATED (US)
FEATURES Location/Qualifiers
source 1..7521
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="cDNA"
BASE COUNT 1879 a 1988 c 1858 g 1796 t
ORIGIN

Query Match 84.9%; Score 1133.8; DB 6; Length 7521;
Best Local Similarity 90.3%; Pred. No. 3.6e-222;
Matches 1238; Conservative 0; Mismatches 97; Indels 36; Gaps 1;
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
DB 2790 GAGGTGCAGCTGGTGGAGTCTGGAGGAGGCTTGGTACAGCCTGGGGTCTCTGAGTCTC 2849
QY 61 TCCTGTGCAGTACCGGATTTCACTTTACGTGGCTACTGGATGTCTCTGGTCCGCCAGGCT 120
DB 2850 TCCTGTGCAGTCTCTGGATTTCACCTTACCTGATTACTACATGAGCTGGTGGTCCGCCAGCT 2909

QY 121 CCAGGAAGGGCTCGAGTGGGTGAATAGATTGAATCTGATATATTGCAACA 180
|||||
Db 2910 CCAGGAAGGACATTGAGTGGTGGCTTGAATAGAAACAAAGCTAATGTTTACAAACA 2969
QY 181 CATTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTTCAAAATCTAGA 240
|||||
Db 2970 GAGTACAGTCATCTGTGAAGGGTCGTTTACCATCTCCAGAGATATTTCCCAAAGCATC 3029
QY 241 CTGTATCTGCAATGACAGCTGAAAACCGAGGACACAGCCGCTGTATTAATCTGTACA --- 297
|||||
Db 3030 CTCTATCTTCAATGAATGCCCTGAGAGCTGAGGACAGTGCCTATTATTACTGTGCAAGA 3089
QY 298 -----GATTTTCATAGACTGGGCCAGGGAACA 324
|||||
Db 3090 GATCCCAATTAATAGATGGTAGTACGAAAGGGTACTTTGACTACTGGGGCCAAAGGTACC 3149
QY 325 CTAGTCAACGCTCTCTCAGCCCTCCACCAAGGGCCCATCGGTCTTCCCTTGGGACCCCTCC 384
|||||
Db 3150 CTGGTCAACGCTCTCTCAGCTGGCCCCAAGGGCCCATCGGTCTTCCCTTGGGACCCCTCC 3209
QY 385 TCCAGAGCAGCTCTGGGGGCACAGCGCCCTGGGCTGCTGTGTCAGAGACTACTTCCCC 444
|||||
Db 3210 TCCAGAGCAGCTCTGGGGGCACAGCGCCCTGGGCTGCTGTGTCAGAGACTACTTCCCC 3269
QY 445 GAACCGGTGACGGTGTCTGTGAATCTCAGCGCCCTGACAGCGCGTGCACACCTTCCCG 504
|||||
Db 3270 GAACCGGTGACGGTGTCTGTGAATCTCAGCGCCCTGACAGCGCGTGCACACCTTCCCG 3329
QY 505 GCTGTCTACAGTCTCTCAGGACTTACTTCCCTCAGCAGCGTGTGACCGTCCCTCCAGC 564
|||||
Db 3330 GCTGTCTACAGTCTCTCAGGACTTACTTCCCTCAGCAGCGTGTGACCGTCCCTCCAGC 3389
QY 565 AGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAAGCCCGACACACCAAGGTG 624
|||||
Db 3390 AGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAAGCCCGACACCAAGGTG 3449
QY 625 GACAAAGATGGAGCCCAATCTTTGTGACAAAATCTCACATGCCACCGTGCCCAAGCA 684
|||||
Db 3450 GACAAAGATGGAGCCCAATCTTTGTGACAAAATCTCACATGCCACCGTGCCCAAGCA 3509
QY 685 CCGTGAATCTGGGGGACCGTCAAGTCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 744
|||||
Db 3510 CCGTGAATCTGGGGGACCGTCAAGTCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT 3569
QY 745 ATGATCTCCCGACCCCTGAGTCAATGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 804
|||||
Db 3570 ATGATCTCCCGACCCCTGAGTCAATGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3629
QY 805 GAGGTCAAGTTCACTGT 864
|||||
Db 3630 GAGGTCAAGTTCACTGT 3689
QY 865 CGGAGGAGCAGTACAAAGCAGCAGTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 924
|||||
Db 3690 CGGAGGAGCAGTACAAAGCAGCAGTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3749
QY 925 GACTGGCTGAATGGCAAGAGTACAAGTGAAGTGTCTTCAAAAGCCCTTCCAGCCCTCC 984
|||||
Db 3750 GACTGGCTGAATGGCAAGAGTACAAGTGAAGTGTCTTCAAAAGCCCTTCCAGCCCTCC 3809
QY 985 ATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGGAGACACAGGTGTACACCTGT 1044
|||||
Db 3810 ATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGGAGACACAGGTGTACACCTGT 3869
QY 1045 CCCCCATCCCGGATGAGTGAACCAAGACAGGTGAGCTGACCTGCTGTGTGTGTGTGTGTGTGTGT 1104
|||||
Db 3870 CCGCCATCCCGGATGAGTGAACCAAGACAGGTGAGCTGACCTGAGCTGTGTGTGTGTGTGTGTGT 3929
QY 1105 TTCTATCCAGGACATCCCGTGGAGTGGGAGAGCAATGGGCGACCCGGAGAACAACTAC 1164
|||||
Db 3930 TTCTATCCAGGACATCCCGTGGAGTGGGAGAGCAATGGGCGACCCGGAGAACAACTAC 3989
QY 1165 AGACACACGCTTCCCGTGTGAGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACC 1224

Db 3990 ARAGACACGCTCCCGTGTGACTCCGACGCTCCTTCTTCTACAGCAAGCTCACC 4049
QY 1225 GTGGCAAGAGCAGGTGGCAGCAGGGGAAGCTTCTCTCATGTCTCGTATGATGAGGCT 1284
|||||
Db 4050 GTGGCAAGAGCAGGTGGCAGCAGGGGAAGCTTCTCTCATGTCTCGTATGATGAGGCT 4109
QY 1285 CTGCAACACCACTACAGCAGAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1335
|||||
Db 4110 CTGCAACACCACTACAGCAGAGAGAGCCCTCTCCCTGTCTCCGGGATCTCTGA 4160
RESULT 9
AX277242 1353 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 27 from Patent WO0175110.
DEFINITION AX277242
ACCESSION AX277242
VERSION AX277242.2 GI:18614077
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Hoogenboom,H.R. and Henderikx,M.P.
TITLE Mucin-1 specific binding members and methods of use thereof
JOURNAL Patent: WO 0175110-A 27 11-OCT-2001;
Dyax Corporation (US)
COMMENT On Feb 7, 2002 this sequence version replaced gi:16548881.
FEATURES
source
1..1353
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="nucleotide sequence coding for amino acid sequence
of seq26"
BASE COUNT 314 a 431 c 376 g 232 t
ORIGIN
Query Match 84.6%; Score 1129.6; DB 6; Length 1353;
Best Local Similarity 91.0%; Pred. No. 2.8e-221;
Matches 1236; Conservative 0; Mismatches 89; Indels 33; Gaps 2;
QY 2 AGTGCAGCTGTGGAGTCTGGGGAGGCTTGTGAAGCCCGGGGGTCCCTTAGACTCT 61
|||||
Db 2 AGGTCCAGCTGTGGAGTCTGGGGAGGCTTGTGACAGCTGGGGTCCCTGAGACTCT 61
QY 62 CCTGTGAGCTAGCGGATTCACCTTTTCTAGTGGCTACTGGATGTCTGGGTCCGCGAGCTC 121
|||||
Db 62 CCTGTGAGCTCTGGATTCACGTTTAGAAGTAACGCCATGGGCTGGTCCGCGAGCTC 121
QY 122 CAGGAAGGGCTCGAGTGGTGTGTAATAGATTGAATCTGATAATTATGCAACAC 181
|||||
Db 122 CAGGAAGGGCTCGAGTGGTGTGTAATAGATTGAATCTGATAATTATGCAACAC 175
QY 182 ATTATCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241
|||||
Db 176 ACTACGAGACTCGTGAAGGGCGGTTCACATCTCCAGAGACATTCACAAAGACGC 235
QY 242 TGTATCTGCAATGAACAGCTTGAACACCGAGGACACAGCCGTGTATTACTGTACAGATT 301
|||||
Db 236 TGTATCTGCAATGAACAGCTTGAACACCGAGGACACAGCCGTGTATTATTGTGCGAAAC 295
QY 302 TCATAG-----ACTGGGGCCAGGGAACACTAGTCACCG 334
|||||
Db 296 ATACCGGGGGGGCGTTTGGACCCCATTTGACTACTGGGGCCAGGGAACCCCTGGTCACCG 355
QY 335 TCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCTTGGCACCCCTCTCCAAAGAGCA 394
|||||
Db 356 TCTCAGGCTCCACCAAGGGCCCATCGGTCTTCCCTTGGCACCCCTCTCCAAAGAGCA 415
QY 395 CCTCTGGGGACAGCGGCCCTTGGCTGGCTGTGTCAGGACTACTTCCCGGACCGGTGA 454
|||||
Db 416 CCTCTGGGGACAGCGGCCCTTGGCTGGCTGTGTCAGGACTACTTCCCGGACCGGTGA 475


```
QY 297 -----AGATTTCATAGACTGGGCGCCAGGGAACACTA 327
Db 431 GATTCTCAAGTTGAGCACTTCTGCCGTATGATCACTTCTGGGGCCAGGGAACCCCTG 490
QY 328 GTACCGCTCTCTCAGCGCTCCACCAAGGCGCCCATCGGTCTTCCCGCTGGCAGCCCTCTCTCC 387
Db 491 GTACCGCTCTCTCAGCGCTCCACCAAGGCGCCCATCGGTCTTCCCGCTGGCAGCCCTCTCTCC 550
QY 388 AAGAGACCTCTGGGGGACAGCGGCGCTGGCTGCCGTGCTCAAGGACTACTTCCCGAA 447
Db 551 AAGAGACCTCTGGGGGACAGCGGCGCTGGCTGCCGTGCTCAAGGACTACTTCCCGAA 610
QY 448 CCGGTGACGCTGTGTGAACCTCAGCGCGCTGACAGCGGCTGCACACCTTCCCGCT 507
Db 611 CCGGTGACGCTGTGTGAACCTCAGCGCGCTGACAGCGGCTGCACACCTTCCCGCT 670
QY 508 GTCTACAGTCTCTAGGACTCTACTCTCCAGCAGCGTGGTGAACCGTCCCTCCAGCAGC 567
Db 671 GTCTACAGTCTCTAGGACTCTACTCTCCAGCAGCGTGGTGAACCGTCCCTCCAGCAGC 730
QY 568 TTGGGCAACCCAGCCTACATCTGCAACGTTGAATCAAGCCCGCAGCAACCAAGGTGAC 627
Db 731 TTGGGCAACCCAGCCTACATCTGCAACGTTGAATCAAGCCCGCAGCAACCAAGGTGAC 790
QY 628 AAGAAAGTGAGCCCAAAATCTTTGTGACAAAACCTCACATGCCACCGTGCACGACCT 687
Db 791 AAGAAAGTGAGCCCAAAATCTTTGTGACAAAACCTCACATGCCACCGTGCACGACCT 850
QY 688 GAACTCGGGGGGACCGCTAGCTCTCTCTCTTCCCGCCCAAAACCAAGCAGCAGCCTCATG 747
Db 851 GAACTCGGGGGGACCGCTAGCTCTCTCTCTTCCCGCCCAAAACCAAGCAGCAGCCTCATG 910
QY 748 ATCTCCCGACCCCTGAGTGCATCTGCTGGTGGAGCTGAGCAGCAGCAAGACCTGAG 807
Db 911 ATCTCCCGACCCCTGAGTGCATCTGCTGGTGGAGCTGAGCAGCAGCAAGACCTGAG 970
QY 808 GTCAAGTTCAACTGTGTACCTGGAGCGCTGGAGGTGCATAATGCCAAGCAAAAGCGCGG 867
Db 971 GTCAAGTTCAACTGTGTACCTGGAGCGCTGGAGGTGCATAATGCCAAGCAAAAGCGCGG 1030
QY 868 GAGGAGCAGTACACAGCAGCTACCGTGTGGTCAAGGCTCCTCAGCGTCTGTGACCAAGAC 927
Db 1031 GAGGAGCAGTACACAGCAGCTACCGTGTGGTCAAGGCTCCTCAGCGTCTGTGACCAAGAC 1090
QY 928 TGCTCAATGGCAAGGAGTACAGTCAAGGTCTCCAAAGAGCCCTCCAGCCCGCCATC 987
Db 1091 TGCTCAATGGCAAGGAGTACAGTCAAGGTCTCCAAAGAGCCCTCCAGCCCGCCATC 1150
QY 988 GAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACCCAGGTGTACACCTTGCC 1047
Db 1151 GAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACCCAGGTGTACACCTTGCC 1210
QY 1048 CCATCCCGGATGAGTGCACCAAGAACAGGTGAGCTGACCTGCTGTGCTCAAGGCTTC 1107
Db 1211 CCATCCCGGATGAGTGCACCAAGAACAGGTGAGCTGACCTGCTGTGCTCAAGGCTTC 1270
QY 1108 TATCCAGCAGCATCCCGTGGAGTGGGAGCAATGGGCGAGCCGCGAGAACACTACAG 1167
Db 1271 TATCCAGCAGCATCCCGTGGAGTGGGAGCAATGGGCGAGCCGCGAGAACACTACAG 1330
QY 1168 ACCAGCCTCCCGTGTGACTCCGAGCGCTCTCTCTCTCTACAGAGCTTCACCGTG 1227
Db 1331 ACCAGCCTCCCGTGTGACTCCGAGCGCTCTCTCTCTCTACAGAGCTTCACCGTG 1390
QY 1228 GACAAGAGCAGGTGGCAGGAGGAGCGTCTTCTATGCTCCGTGATGATGAGGCTG 1287
Db 1391 GACAAGAGCAGGTGGCAGGAGGAGCGTCTTCTATGCTCCGTGATGATGAGGCTG 1450
QY 1288 CACAACCATACAGCAGAGAGCCCTCTCCGTCTCTCCGGGTAATGA 1335
Db 1451 CACAACCATACAGCAGAGAGCCCTCTCCGTCTCTCCGGGTAATGA 1498
```

```
RESULT 11
LOCUS AF019036 1419 bp mRNA linear SYN 03-JAN-2000
DEFINITION Synthetic construct rsv neutralizing human ig gamma chain with
leader mRNA, complete cds.
ACCESSION AF019036
VERSION AF019036.1 GI:6649879
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 1419)
AUTHORS Pilkington,G.R., Gilmour,J.R. and Gilmour,P.S.
TITLE Three dimensional structure of a fully human IgG1, neutralizing
antibody for RSV
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1419)
AUTHORS Pilkington,G.R., Gilmour,J.R. and Gilmour,P.S.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-1997) Intracel Corp., 1871 NW Gilman Blvd,
Issaquah, WA 98027, USA
FEATURES
source Location/Qualifiers
1..1419
/organism="synthetic construct"
/db_xref="taxon:32630"
/clone="pHC2-5#7"
10..1419
/codon_start=1
/transl_table=11
/product="human IgG1 neutralizing heavy chain with leader"
/protein_id="AAF21613.1"
/db_xref="GI:6649880"
/translation="MEFGLSMLFLVALLTGVOCEVOLLRESGDLVOPGRSLRLSCST
SGSFSDYPNWFRQAPGKLEWLGIVRSRLYGTQYAAASVEGRTISRDDSKSTAY
LHNSLKSEDTAVYICGVPVANDIWDGQTLTVSSASTNGSPVFPFLAPSSKSTSGT
AALGLVKDYDFPEPTVSNWNGALTSGVHTFPVAVLSSGLYSLSVTVFSSSLGQT
YICNVNHPKSPNTKDKSLSPKCDKTHTCPCPAPPELLGGPSVFLFPPKPKDITLMS
RTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAAKTPRBEQYNSFVYVSVLTLDHQ
WLANQKCKVKVSKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK
GYPSDIAVEMESNGOGPENNYKTPPVLDSDGGSFELYSLKLTVDKSRWQGNVFCFSVM
HEALNHYTOKSLSLSPGK"
BASE COUNT 326 a 436 c 383 g 274 t
ORIGIN
Query Match 84.4%; Score 1127.2; DB 12; Length 1419;
Best Local Similarity 90.9%; Pred. No. 8.7e-221;
Matches 1227; Conservative 0; Mismatches 108; Indels 15; Gaps 2;
QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 70 GTGCAGCTGCTCAGGAGCTCTGGGGAGACTTGGTACAGCCAGGCGGCTCCTCAGACTC 129
QY 61 TCCTGTGAGCTAGCGGATTCACCTTCAGTGGCTACTGGATGCTCTGGTCCGCCAGGCT 120
Db 130 TCCTGTTCACCTTCAGGATTCAGTTTGGTGACTATCCTGTGAATTTGGTCCGCCAGGCT 189
QY 121 CCAGGGAAGGCGCTCAGCTGGTGGTCTGAAATTAGATTGAATCTGTAATATTATGCAACA 180
Db 190 CCAGGGAAGGCGCTGAGTGGCTAGGTATCCTTTAGAGCAGACTTTATGTTGGGACACTT 249
QY 181 CATTTATCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTAATAAATAGATA 240
Db 250 CAATACGCGCGCTGTGTGAAGGAGATTCACCATCTCAAGAGATGATTCACCAAGCATC 309
QY 241 CTGTATCTGCAATGAACAGCGCTGAAACACCGAGGACAGACCGCGTGTATTACTGT----- 294
Db 310 GCCTATCTGCAATGAACAGCTGAAATCCGAAGACACCGCGGTGTATTATTGTGGGCTA 369
QY 295 -----ACAGATTTTCATAGCTGGGGCCAGGGAACCCCTGGTCAAGCGTCTCCTCAGCCTCC 348
Db 370 CCAAGTGGCTAATCATTTGACTACTTGGGGCCAGGGAACCCCTGGTCAAGCGTCTCCTCAGCCTCC 429
```

```
QY 349 ACCAAGGGCCCATCGGTCTTCCCTCGACCCCTCTCCAAAGAGCACTCTGGGGGCACA 408
Db 430 ACCAAGGGCCCATCGGTCTTCCCTCGACCCCTCTCCAAAGAGCACTCTGGGGGCACA 489
QY 409 GCGGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTCTCGTGAAC 468
Db 490 GCGGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTCTCGTGAAC 549
QY 469 TCAGGCGCCCTGACCAAGCGGGGTGCACACCTTCCCGGCTGTCTACAGTCTCCAGGACTC 528
Db 550 TCAGGCGCCCTGACCAAGCGGGGTGCACACCTTCCCGGCTGTCTACAGTCTCCAGGACTC 609
QY 529 TACTCCCTCAGCAGGCTGGTACCGTGCCTCCAGCAGCTTGGGACCCAGCTACATC 588
Db 610 TACTCCCTCAGCAGGCTGGTACCGTGCCTCCAGCAGCTTGGGACCCAGCTACATC 669
QY 589 TGCAACGTGAATCACAAGCCCAAGCAACACCAAGGTGGACAAGAA---GTGGAGCCCAAA 645
Db 670 TGCAACGTGAATCACAAGCCCAAGCAACACCAAGGTGGACAAGAAAGTTTGAATCCCAAA 729
QY 646 TCTTGTGACAAATCACAATGCCCCAGCGTGCACCACTGAAGTGGCGGGGACCG 705
Db 730 TCTTGTGACAAATCACAATGCCCCAGCGTGCACCACTGAAGTGGCGGGGACCG 789
QY 706 TCAGTCTTCTCTTCCCGCCCAAAACCAAGCAGACACCTCATGATCTCCCGACCCCTGAG 765
Db 790 TCAGTCTTCTCTTCCCGCCCAAAACCAAGCAGACACCTCATGATCTCCCGACCCCTGAG 849
QY 766 GTCACATCGGTGGTGGAGGTGAGCCAGCAGCAACACCTGAGGTCAAGTTCAACTGGTAC 825
Db 850 GTCACATCGGTGGTGGAGGTGAGCCAGCAGCAACACCTGAGGTCAAGTTCAACTGGTAC 909
QY 826 GTGGACGCGTGGAGGTGCATAATGCCAAGACAAGCGCGGGAGGAGCAGTACAACAGC 885
Db 910 GTGGACGCGTGGAGGTGCATAATGCCAAGACAAGCGCGGGAGGAGCAGTACAACAGC 969
QY 886 ACGTACCGTGTGGTCAAGGTCTCAGCGTCTGCACAGGAGTGGCTGAATGGCAAGAG 945
Db 970 ACGTACCGTGTGGTCAAGGTCTCAGCGTCTGCACAGGAGTGGCTGAATGGCAAGAG 1029
QY 946 TACAAGTCAAGGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAACCATCTCCAAA 1005
Db 1030 TACAAGTCAAGGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAACCATCTCCAAA 1089
QY 1006 GCCAAGGGCAGCCCGAGAACCAAGTGTACACCTGCCCCATCCCGGATGAGCTG 1065
Db 1090 GCCAAGGGCAGCCCGAGAACCAAGTGTACACCTGCCCCATCCCGGAGGAGATG 1149
QY 1066 ACCAAGAACCAAGGTACGCTGCTGCTCAAGAGCTTCTATCCAGCGACATCGCC 1125
Db 1150 ACCAAGAACCAAGGTACGCTGCTGCTCAAGAGCTTCTATCCAGCGACATGCTCC 1209
QY 1126 GTGGAGTGGGAGCAATGGCAGCCGAGAACCAACTACAGACCCAGCCCTCCCGTCTG 1185
Db 1210 GTGGAGTGGGAGCAATGGCAGCCGAGAACCAACTACAGACCCAGCCCTCCCGTCTG 1269
QY 1186 GACTCCGAGCGCTCTTCTTCTCTACAGCAAGCTACCGTGGACAAGCAGCGTGGCAG 1245
Db 1270 GACTCCGAGCGCTCTTCTTCTCTATAGCAAGCTACCGTGGACAAGCAGCGTGGCAG 1329
QY 1246 CAGGGGAACGCTTCTTCTATGCTCGGTGATGAGGCTCTGCACAAACCACTACACGAG 1305
Db 1330 CAGGGGAACGCTTCTTCTATGCTCGGTGATGAGGCTCTGCACAAACCACTACACGAG 1389
QY 1306 AAGAGCTCTCCCTGTCTCCGGTAAATGA 1335
Db 1390 AAGAGCTCTCCCTGTCTCCGGTAAATGA 1419

RESULT 12
LOCUS AF027159 1401 bp mRNA linear PRI 16-NOV-1997
DEFINITION Homo sapiens immunoglobulin gamma heavy chain (T6J/g) mRNA, partial
```

```
cds.
AF027159 AF027159.1 GI:2623586
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ohba,H., Kashima,K., Tomozawa,T. and Chiba,J.
1 (bases 1 to 1401)
Molecular expression of human antibody and prediction of
antigen-binding structure (Abstract)
Proc. Jpn. Soc. Immunol. 24, 639 (1994)
2 (bases 1 to 1401)
Ohba,H., Kashima,K., Tomozawa,T. and Chiba,J.
Direct Submission
Submitted (29-SEP-1997) Department of Biological Sciences and
Technology, Science University of Tokyo, 2641 Yamazaki, Noda, Chiba
278, Japan
Location/Qualifiers
1..1401
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TAPC6JC5"
/note="TAPC6JC5 hybridoma was made by fusing an EBV
transformed B cell line, TAPC301-Cl4 with triple
hybridoma, 6JC5"
1..>1401
/gene="T6J/g"
1..>1401
/gene="T6J/g"
/note="anti-HBs antibody; protects chimpanzees from
hepatitis B virus infection"
/codon_start=1
/product="immunoglobulin gamma heavy chain"
/protein_id="AAB86467.1"
/db_xref="GI:2623587"
BASE COUNT 323 a 432 c 380 g 266 t
ORIGIN
Query Match 84.2%; Score 1124.2; DB 9; Length 1401;
Best Local Similarity 91.0%; Pred. No. 3.6e-220;
Matches 1227; Conservative 0; Mismatches 98; Indels 24; Gaps 2;
QY 2 AGGTGACGCTGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGTCCTTACACTCT 61
Db 59 AGGTGACGCTGTGGAGTCTGGGGAGGCTGTGCCAGCTGGAGGTCCTTGACACTCT 118
QY 62 CTTGTGCACTAGCGGATTCACCTTTAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCTC 121
Db 119 CTTGTGACCTCTGGATTACCTTTACCTTATGATCTATGATCTGATTAATATGCAACAC 178
QY 122 CAGGGAAGGGCTCGAGTGGGTTCGTAATAGATTGAAATCTGATTAATATGCAACAC 181
Db 179 CAGGGAAGGGCTCGAGTGGGTTCGTAATAGATTGAAATCTGATTAATATGCAACAC 232
QY 182 ATTATCGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATCAAAATCTAGAC 241
Db 233 ATAAGTAGACTCCATGAAGGCCGACTACCATCTCCAGAGACAATCCCAAGACAGC 292
QY 242 TGTATCTCAATGAACAGCCTGAAACCGAGGACACAGCCGCTGTATTACTG----- 293
Db 293 TGTATTTGAAATGAACAGCCTGACAGCTGAGGACACGCTGTGTATTACTGTGCGAGGA 352
```

```
QY 294 -----TACAGATTTCATAGACTGGGCCAGGACACTAGTCTACCGTCTCTCTCAG 343
Db 353 CAGCTTGCTTTAACGCTATGACTTCTGGGGCCAGGAACTGCTACCGTCTCTCAG 412
QY 344 CTTCCACCAAGGCCATCGTCTTCCGCCCTGGCACCCTCTCCCAAGAGCAGCTCTGGGG 403
Db 413 CTTCCACCAAGGCCATCGTCTTCCGCCCTGGCACCCTCTCCCAAGAGCAGCTCTGGGG 472
QY 404 GCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAAACCGGTGAGGCTGCT 463
Db 473 GCACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAAACCGGTGAGGCTGCT 532
QY 464 GGAACCTCAGCGCCCTGACAGCGGCTGCACACCTTCCCGGCTGCTCCTACAGTCTCTCAG 523
Db 533 GGAACCTCAGCGCCCTGACAGCGGCTGCACACCTTCCCGGCTGCTCCTACAGTCTCTCAG 592
QY 524 GACTCTACTCTCCCTCAGCAGCTGGTGACCGTCCCTCCAGCAGCTTGGCACCAGACT 583
Db 593 GACTCTACTCTCCCTCAGCAGCTGGTGACCGTCCCTCCAGCAGCTTGGCACCAGACT 652
QY 584 ACATCTGCAACGCTGAATCAACAGCCAGCAACCAAGGTGCACAAAGTGGAGCCCA 643
Db 653 ACATCTGCAACGCTGAATCAACAGCCAGCAACCAAGGTGCACAAAGTGGAGCCCA 712
QY 644 AATCTTGTGACAAACTCACATGCCCGCCACCGTGCACACCTGAACCTCCGCGGGGCAC 703
Db 713 AATCTTGTGACAAACTCACATGCCCGCCACCGTGCACACCTGAACCTCCGCGGGGCAC 772
QY 704 CGTCAGTCTTCTCTTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTG 763
Db 773 CGTCAGTCTTCTCTTCCCGCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTG 832
QY 764 AGGTACATCGCTGGTGGTGGAGCTGAGCCAGCAAGACCTCAGTCAAGTTCACACTGCT 823
Db 833 AGGTACATCGCTGGTGGTGGAGCTGAGCCAGCAAGACCTCAGTCAAGTTCACACTGCT 892
QY 824 ACCTGGACGCGCTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTCAACA 883
Db 893 ACCTGGACGCGCTGGAGGTGCATAATGTTAAGACAAAGCCGCGGAGGAGCAGTCAACA 952
QY 884 GCAGCTACCGTGTGTCACGCTCTCTCAGCGTCTCTGACCAAGACACTGGCTGAATGCGCAGG 943
Db 953 GCAGCTACCGTGTGTCACGCTCTCTCAGCGTCTCTGACCAAGACACTGGCTGAATGCGCAGG 1012
QY 944 AGTACAAGTGCAGAGTCTCCAAAGACCTCCCGACGCCCATCGAGAAACCATCTCCA 1003
Db 1013 AGTACAAGTGCAGAGTCTCCAAAGACCTCCCGACGCCCATCGAGAAACCATCTCCA 1072
QY 1004 AAGCCAAAGGGCAGCCCGCAGAACACAGGTGTACACCTGCCCCCATCCCGGGATGAGC 1063
Db 1073 AAGCCAAAGTGCAGCCCGCAGAACACAGGTGTACACCTGCCCCCATCCCGGGATGAGC 1132
QY 1064 TGACCAAGAACACAGTCAAGCTGACCTGCTGGTCAAGGCTTCTATCCAGCGACATCG 1123
Db 1133 TGACCAAGAACACAGTCAAGCTGACCTGCTGGTCAAGGCTTCTATCCAGCGACATCG 1192
QY 1124 CCGTGGAGTGGAGAGCAATGGCAGCCGAGAACCAACTACAAAGACACAGCCCTCCCGTGC 1183
Db 1193 CCGTGGAGTGGAGAGCAATGGCAGCCGAGAACCAACTACAAAGACACAGCCCTCCCGTGC 1252
QY 1184 TGGACTCCGACGCGCTCTTCTTCTTCTACAGCAAGCTCACCGTGCAGACAGCAGTGGC 1243
Db 1253 TGGACTCCGCTCGGCTCTTCTTCTTCTTCTACAGCAAGCTCACCGTGCAGACAGCAGTGGC 1312
QY 1244 AGCAGGGGACGCTCTTCTTCTTCTGCTGATGCTGATGAGCTCTGACACACCACTACAGC 1303
Db 1313 AGCAGGGGACGCTCTTCTTCTTCTGCTGATGCTGATGAGCTCTGACACACCACTACAGC 1372
QY 1304 AGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1332
Db 1373 AGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1401
```

```
RESULT 13
AK093806
LOCUS
DEFINITION
  Homo sapiens cDNA FLJ36487 fis, clone THYMU2017844, highly similar
  to Homo sapiens mRNA for immunoglobulin lambda heavy chain.
ACCESSION
  AK093806
VERSION
  AK093806.1 GI:21752738
KEYWORDS
  oligo capping; fis (full insert sequence);
SOURCE
  Homo sapiens shymus cDNA to mRNA, clone_lib:THYMU2
  clone:THYMU2017844.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1
  Ishibashi, T., Kanehori, K., Yosida, M., Watanabe, S., Ishida, S.,
  Ono, Y., Hotuta, T., Hiraoka, S., Murakawa, K., Takiguchi, S.,
  Kusano, J., Watanabe, M., Fujimori, K., Tanai, H., Ishida, M.,
  Yamashita, H., Chiba, Y., Sugiyama, T., Irie, R., Otsuki, T., Sato, H.,
  Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
  Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K.,
  Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M.,
  Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y.,
  Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
  NEDO human cDNA sequencing project
  Unpublished
  2 (bases 1 to 1642)
  Isogai, T. and Yamamoto, J.
  Direct Submission
  Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
  Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
  (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
  NEDO human cDNA sequencing project supported by Ministry of
  Economy, Trade and Industry of Japan; cDNA full insert sequencing:
  Research Association for Biotechnology (RAB); cDNA library
  construction: Helix Research Institute (HRI) (supported by Japan
  Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
  HRI, and Biotechnology Center, National Institute of Technology and
  Evaluation; clone selection for full insert sequencing: HRI and
  RAB; annotation: HRI and RAB.
FEATURES
  source
    Location/Qualifiers
    1..1642
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="THYMU2017844"
      /tissue_type="shymus"
      /clone_lib="THYMU2"
      /note="cloning vector: pME18SFL3"
    81..1517
      /note="unnamed protein product"
      /codon_start=1
      /protein_id="BAC04226.1"
      /db_xref="GI:21752739"
      /translation="MEFGLSWVYLKVGQCVHLVSGGDLVQPGRSRLRLSCTVLS
      GFARGDYAMAWVRQAFKGLWYALITNNARGATEHASSVRGRTISGDDSKNTAYL
      QMNSLKTEDTGRYCYAVVYDYGNNRRDADFVWGQGTMLVSSASGKGSFPLA
      PSSKSTSGGTAALCLVKDYFPEPTVSWNSGALTGVHTFPAVLGSSGLYLSVST
      VPSSSLGTOTYICNVNHPKSTKVDKRVPEKSDCKTHTCPQAPAPLGGPSVLPFP
      KPDKTLMISHTPEVTCVVDVSHEDPEVKFNWYDGVENVNKTAKPREQYNSTYRV
      SVLTIVLHQQWLNGKEYKCVSNKALPAIEKTSKAGQGPREFQVITLPPSREMTKN
      QVSLTCLVKGFPDSDIAVWESNGQPNENYKTTTPPVLDSDGSGFFLYSLKTVDRKMQQ
      -GNVFSQVMHEALHNHYTKLSLSPGK"
  BASE COUNT
    377 a 509 c 450 g 306 t
  ORIGIN
    Query Match 84.1%; Score 1123.4; DB 9; Length 1642;
    Best Local Similarity 89.8%; Pred. No. 5.2e-220;
    Matches 1236; Conservative 0; Mismatches 96; Indels 45; Gaps 1;
    QY 4 GTGCAGCTGGTGGAGCTCTGGGGGAGGCTTGCTGAAGCCCGGGGCTCCCTAGACTCTCC 63
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
    Db 141 GTGCACCTGGTGGAGCTCTGGGGGAGACTTGCTGCAGCAGCGGCGGTCCCTGAGACTCTCC 200
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
    QY 64 TGTGCAGCTAGCGGATTCACTTTCAGTGGCTACTGGATGCTCTGGGTCCGCCAGGCTCCA 123
```

```
Db 201 TGTACAGTCTCTGGAATCGCCCGTGGTGATATGCGCATGGCCCTGGGTCCGCCAGGCTCCA 260
Qy 124 GGAAGAGGGCTCGAGTGGTGGTGAATAGATTGAATCTGATAATATGCAACACAT 183
Db 261 GGAAGAGGGCTGGAGTGGTGGTGGATGAACAATAATGCTCGAGGTGGGGCAACAGAG 320
Qy 184 TATGCGGAGTCTGTGAAGGGAATATCACCATCTCAAGAGATGATTCAAAATCTAGACTG 243
Db 321 CACGCTCGTCTGTGAGAGCAGATTCAACCATCTCAGGAGATGATTCCAAAAACATCGCC 380
Qy 244 TATCTGCAATGAACAGCCTGAAACCGGAGACACAGCCGTGATTACTGTAC----- 296
Db 381 TATCTGCAATGAACAGCCTGAAACCGGAGACACAGCCGTGATTACTGTGTAGAGTC 440
Qy 297 -----AGATTTCATAGACTGGGCCAG 318
Db 441 GTCTATTATTATGATAGTGTGTAACCGTAGGAGAGATGCTTTTGTCTGGGCCAA 500
Qy 319 GGAACACTAGTACCGCTCTCTCAGCCTCCACCAAGGGCCATCGGTCTTCCCCCTGGCA 378
Db 501 GGAACAATGGTCTCGTCTCTCAGCCTCCACCAAGGGCCATCGGTCTTCCCCCTGGCA 560
Qy 379 CCTCTCCAGAGCAGCCTCTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTAC 438
Db 561 CCTCTCCAGAGCAGCCTCTGGGGCACAGCGCCCTGGCTGCTGGTCAAGGACTAC 620
Qy 439 TTCCCCGAACCGGTGAGCGTGTGTGAACCTCAGGGGCCCTGACCAGCGCGTGCACACC 498
Db 621 TTCCCCGAACCGGTGAGCGTGTGTGAACCTCAGGGCCCTGACCAGCGCGTGCACACC 680
Qy 499 TTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC 558
Db 681 TTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGC 740
Qy 559 TCCAGCAGCTTGGSCACCCAGACCTACATCTGCAAGTGAATCACAGCCAGCAACACC 618
Db 741 TCCAGCAGCTTGGSCACCCAGACCTACATCTGCAAGTGAATCACAGCCAGCAACACC 800
Qy 619 AAGTGTGACAAGAAGTGGAGGCCAAATCTTTGTGACAAAACCTCACACATGCCACCCTGC 678
Db 801 AAGTGTGACAAGAAGTGGAGGCCAAATCTTTGTGACAAAACCTCACACATGCCACCCTGC 860
Qy 679 CCAGCAGCTGAAGTCCGGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 738
Db 861 CCAGCAGCTGAAGTCCGGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 920
Qy 739 ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTGAGCCACGAA 798
Db 921 ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTGAGCCACGAA 980
Qy 799 GACCTGAGGTCAAGTTCAATGGTACGTGGAGCGCGGTGGAGGTGCATATGCCAAGACA 858
Db 981 GACCTGAGGTCAAGTTCAATGGTACGTGGAGCGCGGTGGAGGTGCATATGCCAAGACA 1040
Qy 859 AAGCCGGGGAGGAGCAGTACACAGCAGCTACCGTGTGCTGAGCGTCTCACCCCTCTG 918
Db 1041 AAGCCGGGGAGGAGCAGTACACAGCAGCTACCGTGTGCTGAGCGTCTCACCCCTCTG 1100
Qy 919 CACCAGGACTGGCTGAATGCAAGGAGTACAAGTGAAGTCTCCAACAAAGCCCTCCCA 978
Db 1101 CACCAGGACTGGCTGAATGCAAGGAGTACAAGTGAAGTCTCCAACAAAGCCCTCCCA 1160
Qy 979 GCCCCCCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACACACAGGTGTAC 1038
Db 1161 GCCCCCCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACACACAGGTGTAC 1220
Qy 1039 ACCCTGCCCCATCCCGGGATGAGTGCACCAAGACAGGTGACCTGACCTGCCTGGTC 1098
Db 1221 ACCCTGCCCCATCCCGGGAGGAGTGCACCAAGACAGGTGACCTGACCTGCCTGGTC 1280
Qy 1099 AAAGGCTTCTATCCAGCAGACATCGCCGTGGAGTGGGAGAGCAATGGGACCGCGAGAAC 1158
|||||
```

```
Db 1281 AAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAAC 1340
Qy 1159 AACTACAAGACACCGCTCCCGTGTGGACTCCGACGGCTCTCTTCTCTCTACAGCAAG 1218
Db 1341 AACTACAAGACACCGCTCCCGTGTGGACTCCGACGGCTCTCTTCTCTCTATAGCAAG 1400
Qy 1219 CTCACCGTGGACAAGACAGAGGTGGCAGCAGGGAACGCTTCTCTCATGTCTCCGATGAT 1278
Db 1401 CTCACCGTGGACAAGACAGAGGTGGCAGCAGGGAACGCTTCTCTCATGTCTCCGATGAT 1460
Qy 1279 GAGGCTCTGCACAACCACTACAGCAGAGAGCCCTCTCCCTGTCTCCCGGTAATGA 1335
Db 1461 GAGGCTCTGCACAACCACTACAGCAGAGAGCCCTCTCCCTGTCTCCCGGTAATGA 1517

RESULT 14
HSIGILH HSIGILH 1673 bp mRNA linear PRI 19-AUG-1998
LOCUS Homo sapiens mRNA for immunoglobulin lambda heavy chain.
DEFINITION Y14737
ACCESSION Y14737
VERSION Y14737.1 GI:2765424
KEYWORDS constant region; IgG1; immunoglobulin; lambda heavy chain; variable
region.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1673)
Paterson,T., Innes,J., McMillan,L., Downing,I. and Carter,M.C.
Variation in IgG1 heavy chain allotype does not contribute to
differences in biological activity of two human anti-Rhesus (D)
monoclonal antibodies
JOURNAL Immunotechnology 4 (1), 37-47 (1998)
MEDLINE 98326459
PUBMED 9661813
REFERENCE
2 (bases 1 to 1673)
Paterson,T.
Direct Submission
JOURNAL Submitted (03-SEP-1997) T. Paterson, National Science Laboratory,
Scottish Nat. Blood Transfusion Service, 12 Bristo Place,
Edinburgh, EH1 1EZ, Scotland, UK
FEATURES
Location/Qualifiers
1..1673
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="human /mouse
LHM70/45.3 (THERAD 06)"
66..1499
/gene="IgG1L"
66..1499
/gene="IgG1L"
/codon_start=1
/product="immunoglobulin lambda heavy chain"
/db_xref="GI:2765425"
/translation="MERSLVFLVLRGVQCVQLVESGGGVQVQPSRLRLSCANS
GTFPSNTGPMHWROAPGKGLVAAIWDGSKNYIADSVGRFTISDNSKNTLYMQM
NSLRADTAVYICAREGRWRYTFTVTIGYFDYVGGQTLVTVSSASTKGPSVFPPLAP
SSKSTSGTGAALGCLVKDYFPEPTVYSWNSGALTSGVHPFPAVLQSSGLYSLSSVTV
PSSSLGTQTYICNVNHPKSNTKVDKRVKPSCKDTHTCPPCAPPELLGGPSVFLFPPK
PKDTLMISRTPEVTCVVVDVSHEDPEVKYNNVYDGVVHNKATKPREQYNSYRVVS
VLTVLHQDLNKGKEYCKVSNKALPAPIEKTIISKAKQGPQVYITLPPSREMTKNQ
VSLTCLVKFGYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSLYTKVDSRWQOG
NVFSCSVNHEALHNHYTQKSLSLSPGK"
66..122
/sig_peptide
123..1496
/mat_peptide
/gene="IgG1L"
/product="Immunoglobulin lambda heavy chain"
123..509
/V_region
/gene="IgG1L"
/product="Immunoglobulin lambda heavy chain variable
region"
```

[illegible]

Db 158 GAAGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTACAGCTGGCAGGTCCTCGAGACTC 217
QY 61 TCCTGTGCAGCTAGCGGATTCACATTTTCAGTGGCTACTGGATGCTCGTGGTCCGCCAGGCT 120
Db 218 TCCTGTGCAGCTCTGGATTCACCTTTTAATGATTATGCCATGCACTGGGTCCGCCAAGCT 277
QY 121 CAGGGAAGGGCTCGAGTGGGTTCGTAATTAAGATTGAATCTGATAATTAATGCAACA 180
Db 278 CCAGGGAAGGGCTGGAGTGGGTCTCAGGTATATAAGTTGG-----GATAGTAGTAGTATA 331
QY 181 CATTATGGGAGTCTGTGAAGGGGAATTCACCATTCTCAAGAGATGATTTCAAAATCTAGA 240
Db 332 GGCTATGGGACTCTGTGAAGGGCCGATTACCATTCTCCAGAGACAACGCCAAGACTCC 391
QY 241 CTGTATCTGCAAAATGAACAGCTTGAAGCCGAGGACACAGCCGTGTATTACTGTACAGAT 300
Db 392 CTGTATCTGCAAAATGAACAGTCTGAGAGCTGAGGACATGSCCTTATATTACTGTGTAAA 451
QY 301 TTCATAGA-----CTGGGGCCAG 318
Db 452 GGCAGAGATTACTATGATAGTGGTGTATTTCACGGTTGCTTTTGATATCTGGGGCCAA 511
QY 319 GGAACACTAGTCAACCTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCTCCCTGGCA 378
Db 512 GGGACAATGTCACCGTCTCTTCAAGCTCCACCAAGGGCCCATCGGTCTTCCCTCCCTGGCA 571
QY 379 CCCTCTCTCCAAAGACACCTCTGGGGGCACAGCGGCCCTGGGCTGCCGTGTCGAAGACTAC 438
Db 572 CCCTCTCTCCAAAGACACCTCTGGGGGCACAGCAGCCCTGGGCTGCCGTGTCGAAGACTAC 631
QY 439 TTCCCGCAACCGGTGACGGTGTCTGGAACCTCAGGGGCCCTGACCGCCCTGACCGCGTGCACAC 498
Db 632 TTCCCGCAACCGGTGACGGTGTCTGGAACCTCAGGGGCCCTGACCGCGCGTGCACAC 691
QY 499 TTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCC 558
Db 692 TTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCC 751
QY 559 TCCAGCAGCTTGGCCACCCAGACTACATCTGAAGTGAATCACAAGCCCGCAGCAACACC 618
Db 752 TCCAGCAGCTTGGCCACCCAGACTACATCTGAAGTGAATCACAAGCCCGCAGCAACACC 811
QY 619 AAGTGGACAAAGATGGAGCCCAATCTGTGACAAACTCACACATGCCACCGCTGC 678
Db 812 AAGTGGACAAAGATGGAGCCCAATCTGTGACAAACTCACACATGCCACCGCTGC 871
QY 679 CCAGCAGCTGAATTCGGGGGGCACCGTCACTCTCTTCCCTCCCAAAACCCCAAGGAC 738
Db 872 CCAGCAGCTGAATTCCTTGGGGGACCGTCACTCTCTTCCCTCCCAAAACCCCAAGGAC 931
QY 739 ACCCTCATGATCTCCCGGACCCCTGAGGTCACTGCTGGTGGTGGACGTGAGCCACGAA 798
Db 932 ACCCTCATGATCTCCCGGACCCCTGAGGTCACTGCTGGTGGTGGACGTGAGCCACGAA 991
QY 799 GACCTGAGTCAAGTTCAACTGGTACGTGGAGCGGCTGAGGTGCATTAATGCCAAGACA 858
Db 992 GACCTGAGTCAAGTTCAACTGGTGGAGCGGCTGGAGGTGCATTAATGCCAAGACA 1051
QY 859 AAGCCGGGGAGGAGGAGTACACAGCAGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 918
Db 1052 AAGCCGGGGAGGAGGAGTACAACTCCAGGTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1111
QY 919 CACGAGACTGGCTGAATGGCAAGGAGTACAGTGCAGGCTCTCCAAACAAAGCCCTCCCA 978
Db 1112 CACGAGACTGGCTGAATGGCAAGGAGTACAGTGCAGGCTCTCCAAACAAAGCCCTCCCA 1171
QY 979 GCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCCACAGGTGTAC 1038
Db 1172 GCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCCACAGGTGTAC 1231
QY 1039 ACCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCCAGGTGACCTGCCTGGTGC 1098
Db 1232 ACCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCCAGGTGACCTGCCTGGTGC 1291

QY 1099 AAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGCAGCCCGAGAAC 1158
Db 1292 AAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGAGCCCGAGAAC 1351
QY 1159 AACTACAAGACCACGCTCTCCCGTGTGGACTCCGACGGCTCTCTCTCTACAGCAAG 1218
Db 1352 AACTACAAGACCACGCTCTCCCGTGTGGACTCCGACGGCTCTCTCTCTACAGCAAG 1411
QY 1219 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGTCTCCGTGATGAT 1278
Db 1412 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGTCTCCGTGATGAT 1471
QY 1279 GAGGCTTCTGCACAAACACTTACACGAGAGAGCCCTCTCCCTGTCTCCGGTAAATGA 1335
Db 1472 GAGGCTTCTGCACAAACACTTACACAGAGAGCCCTCTCCCTGTCTCCGGTAAATGA 1528

Search completed: April 26, 2003, 06:31:23
Job time : 2682.46 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: April 26, 2003, 04:55:21 ; Search time 1766.31 seconds
(without alignments)
12240.775 Million cell updates/sec

Title: US-09-674-716B-18
Perfect score: 1335

Sequence: 1 gaagtgcagctggtggagtc.....ccctgtctccgggtaaatga 1335

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estro.*
7: em_estro.*
8: em_estro.*
9: gb_est1.*
10: gb_est2.*
11: gb_est3.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
21: em_gss_vrt.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	898.8	67.3	1020	14	BQ062878
2	860.8	64.5	947	14	BQ709771
3	847.2	63.5	958	14	BQ706140
4	839.2	62.9	926	12	BG755166
5	835.4	62.6	988	14	BQ708857
6	831.2	62.3	901	13	BM007892

7	826.4	61.9	918	14	BQ708022	AGENCOURT
8	821.2	61.5	1029	14	BQ063185	AGENCOURT
9	819.6	61.4	887	14	BQ711255	AGENCOURT
10	819.6	61.4	995	14	BM914540	AGENCOURT
11	805.6	60.3	881	14	BQ711291	AGENCOURT
12	797	59.7	1031	14	BQ064886	AGENCOURT
13	794.2	59.5	936	14	BQ711727	AGENCOURT
14	792.8	59.4	940	14	BQ705928	AGENCOURT
15	788	59.0	980	14	BM914504	AGENCOURT
16	787.4	59.0	977	14	BQ710532	AGENCOURT
17	782	58.6	843	13	BM007897	AGENCOURT
18	780.4	58.5	991	14	BQ708936	AGENCOURT
19	777.6	58.2	930	13	BM007597	AGENCOURT
20	774	58.0	973	14	BQ706204	AGENCOURT
21	772.2	57.8	981	14	BM914528	AGENCOURT
22	765.4	57.3	926	14	BQ710304	AGENCOURT
23	761	57.0	917	14	BQ708169	AGENCOURT
24	758.2	56.8	945	14	BQ712403	AGENCOURT
25	756.2	56.6	961	14	BQ710233	AGENCOURT
26	752	56.3	783	13	BM007838	AGENCOURT
27	749.6	56.1	895	14	BQ708303	AGENCOURT
28	749.2	56.1	1012	14	BM914556	AGENCOURT
29	747.6	56.0	1026	14	BM914288	AGENCOURT
30	740.4	55.5	913	14	BQ707472	AGENCOURT
31	738.2	55.3	914	14	BQ712363	AGENCOURT
32	737.6	55.3	906	14	BQ711709	AGENCOURT
33	730.6	54.7	944	14	BQ712397	AGENCOURT
34	730.4	54.7	919	14	BQ709339	AGENCOURT
35	729.6	54.7	936	14	BQ707530	AGENCOURT
36	728.6	54.6	1014	14	BM914505	AGENCOURT
37	727.4	54.5	855	13	BM007689	AGENCOURT
38	727.2	54.5	973	14	BQ708902	AGENCOURT
39	726.8	54.4	870	12	BG757815	AGENCOURT
40	726.4	54.4	888	12	BG757604	AGENCOURT
41	725.6	54.4	941	14	BQ712021	AGENCOURT
42	725.4	54.3	925	14	BQ709853	AGENCOURT
43	725.2	54.3	991	14	BQ707621	AGENCOURT
44	724.8	54.3	908	13	BM007718	AGENCOURT
45	723.2	54.2	932	14	BQ709560	AGENCOURT

ALIGNMENTS

RESULT 1
BQ062878
LOCUS BQ062878 1020 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT_6826949 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924420
5', mRNA sequence.
ACCESSION BQ062878
VERSION BQ062878.1 GI:19890085
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1020)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LICM2094 row: h column: 21
High quality sequence start: 21
High quality sequence stop: 681.
Location/Qualifiers

[illegible]

QY 1122 GCCTGTGAGTGGAGAGCAATGGCAGCGGAGAAACAACCTACAAGACCGCTCCCGT 1181
 DB 671 GCGGTGGAGTGGAGAGCAATGGCAGCGGAGAAACAACCTACAAGACCGCTCCCGT 730
 QY 1182 GCTGACATCCGACGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAGACGAGTG 1241
 DB 731 GCTGACATCCGACGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAGACGAGTG 790
 QY 1242 GCAGCAGGGGAACGCTTCTCTCATGCTCGTGATGCATGAGGCTCTGCACAACTACTAC 1301
 DB 791 GCAGCAGGGGAACGCTTCTCTCATGCTCGTGATGCATGAGGCTCTGCACAACTACTAC 850
 QY 1302 GCAG-AGAGAGCTCTCCCTGTCTCCGGGTAA 1332
 DB 851 ACAGAAAGAGCTCTCCCTGTCTCCGGGTAA 882

RESULT 4
 BG755166 926 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602711488F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4852076 5',
 mRNA sequence.
 ACCESSION BG755166
 VERSION BG755166.1 GI:14065819
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 926)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cqabps-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1CM1695 row: 0 column: 21
 High quality sequence stop: 888.
 Location/Qualifiers
 1..926
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4852076"
 /clone_lib="NIH_MGC_48"
 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: B-cells; Vector: pGB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected
 for average insert size 1.8kb. Library constructed by Ling
 Hong in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 225 a 309 c 244 g 148 t
 ORIGIN

Query Match 62.9%; Score 839.2; DB 12; Length 926;
 Best Local Similarity 97.9%; Pred. No. 2.7e-192;
 Matches 850; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 468 CTCAGGGCCCTGACAGCGCGGTGCACACTTCCCGGCTGCTCTACAGTCTCAGGACT 527
 DB 2 CTCAGGGCCCTGACAGCGCGGTGCACACTTCCCGGCTGCTCTACAGTCTCAGGACT 61
 QY 528 CTACTCCTCTCAGACGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCCACCCAGACCTACAT 587

DB 62 CTACTCCTCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT 121
 QY 588 CTGCAACGTGAATCACAAGCCGAGCAACACCAAGAGTGGACAAGAGTGGAGCCCAATC 647
 DB 122 CTGCAACGTGAATCACAAGCCGAGCAACACCAAGAGTGGACAAGAGTGGAGCCCAATC 181
 QY 648 TTGTGACAAAACCTACACATGCCCACCGTGGCCAGCACCTGAACCTCGCGGGGACCGTC 707
 DB 182 TTGTGACAAAACCTACACATGCCCACCGTGGCCAGCACCTGAACCTCTCTGGGGGACCGTC 241
 QY 708 AGTCTTCTCTTCCCTCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGT 767
 DB 242 AGTCTTCTCTTCCCTCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGT 301
 QY 768 CACATCGGTGGTGGAGCTGAGCCACCAAGACCCCTGAGGTCAAGTTCAACTGGTACGT 827
 DB 302 CACATCGGTGGTGGAGCTGAGCCACCAAGACCCCTGAGGTCAAGTTCAACTGGTACGT 361
 QY 828 GGACGGCGTGGAGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAC 887
 DB 362 GGACGGCGTGGAGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAC 421
 QY 888 GTACCGTGTGGTCAGCGTCTCTACCGTCTCTGACACGAGACTGGCTGAATGGCAAGAGTA 947
 DB 422 GTACCGTGTGGTCAGCGTCTCTACCGTCTCTGACACGAGACTGGCTGAATGGCAAGAGTA 481
 QY 948 CAAAGTCAAGGTCTCCCAACAAAGCCCTCCACGCCCATCTCGAGAAACCATCTCCAAAGC 1007
 DB 482 CAAAGTCAAGGTCTCCCAACAAAGCCCTCCACGCCCATCTCGAGAAACCATCTCCAAAGC 541
 QY 1008 CAAAGGGCAGCCCGGAGAACACACAGGTGTACACCTGCCCTCCCGGATGAGCTGAC 1067
 DB 542 CAAAGGGCAGCCCGGAGAACACACAGGTGTACACCTGCCCTCCCGGATGAGCTGAC 601
 QY 1068 CAAAGACCAAGTCAAGCTGACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1127
 DB 602 CAAAGACCAAGTCAAGCTGACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 661
 QY 1128 GGAGTGGGAGAGCAATGGGAGCGGAGAACAACTACAAGACACACGCTCCCGTGTGTGGA 1187
 DB 662 GGAGTGGGAGAGCAATGGGAGCGGAGAACAACTACAAGACACACGCTCCCGTGTGTGGA 721
 QY 1188 CTCGACGGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGCA 1247
 DB 722 CTCGACGGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGCA 781
 QY 1248 GGGGAACGCTTCTCTCATGCTCCGCTGATGCATGAGGCTCTGACACACCACTACACGAGAA 1307
 DB 782 GGGGAACGCTTCTCTCATGCTCCGCTGATGCATGAGGCTCTGACACCACTACACGAGAA 841
 QY 1308 GAGCCTCTCTCCCTGTCTCCCGGTAAATGA 1335
 DB 842 AAAGCCTCTCTCTCTCCCGGTAAATGA 869

RESULT 5
 BG708857 988 bp mRNA linear EST 16-JUL-2002
 DEFINITION AGENCOURT_8352194 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277561
 5', mRNA sequence.
 ACCESSION BG708857
 VERSION BG708857.1 GI:21847756
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 988)
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2464 row: c column: 02
High quality sequence stop: 716.
Location/Qualifiers
source
1. .988
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6277561"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT 230 a 338 c 258 g 162 t
ORIGIN
Query Match 62.6%; Score 835.4; DB 14; Length 988;
Best Local Similarity 95.6%; Pred. No. 2.3e-191;
Matches 903; Conservative 0; Mismatches 36; Indels 6; Gaps 4;
QY 308 ACTGGGCGGAGGACACTAGTCTCCTCAGCTCTCCACCAAGGCGCCATCGGTCT 367
Db 16 ACTGGGCGGAGGACACTAGTCTCCTCAGCTCTCCACCAAGGCGCCATCGGTCT 75
QY 368 TCCCGCTGGACCTCTCCAAAGACACCTCTGGGGGACAGCGCCCTGGGCTGG 427
Db 76 TCCCGCTGGACCTCTCCAAAGACACCTCTGGGGGACAGCGCCCTGGGCTGG 135
QY 428 TCAAGGACTACTTCCCGAACCGTGAGGCTGTGGAACTCAGGCGCCCTGACCAAGC 487
Db 136 TCAAGGACTACTTCCCGAACCGTGAGGCTGTGGAACTCAGGCGCCCTGACCAAGC 195
QY 488 GCGTGCACACCTTCCCGGCTCTCTACAGTCTCTCAGGACTCTACTCTCCTCAGCAGCGTGG 547
Db 196 GCGTGCACACCTTCCCGGCTCTCTACAGTCTCTCAGGACTCTACTCTCCTCAGCAGCGTGG 255
QY 548 TGACCGTCCCTCCAGCAGCTGGGCGCCAGACCTACATCTGCAAGTGAATCACAAGC 607
Db 256 TGACCGTCCCTCCAGCAGCTGGGCGCCAGACCTACATCTGCAAGTGAATCACAAGC 315
QY 608 CCAGCAACCAAGGTGGACAAAGTGGAGCCCAATCTGTGACAAAACCTCACACAT 667
Db 316 CCAGCAACCAAGGTGGACAAAGTGGAGCCCAATCTGTGACAAAACCTCACACAT 375
QY 668 GCCACCGTCCCGCAGCAGCTGAATCTCGGGGGCAGCGTCAGTCTTCTCTTCCCGCCAA 727
Db 376 GCCACCGTCCCGCAGCAGCTGAATCTCGGGGGCAGCGTCAGTCTTCTCTTCCCGCCAA 435
QY 728 AACCAAGGACACCTCATGATCTCCGGGACCCCTCAGGTCACATCGGTGGTGGAGC 787
Db 436 AACCAAGGACACCTCATGATCTCCGGGACCCCTCAGGTCACATCGGTGGTGGAGC 495
QY 788 TGAGCAGGAGACCTGAGGTCAAGTTCAACTGTGAGGCGGTGAGGTGCATA 847
Db 496 TGAGCAGGAGACCTGAGGTCAAGTTCAACTGTGAGGCGGTGAGGTGCATA 555
QY 848 ATGCCAAGCAAAAGCCGGGAGGAGGAGTACAAACAGCAGCTACCGTGTGGTCAGCGTCC 907
Db 556 ATGCCAAGCAAAAGCCGGGAGGAGGAGTACAAACAGCAGCTACCGTGTGGTCAGCGTCC 615
QY 908 TCACCGTCTCCACGAGGACTGGCTGAATGCCAAGGAGTACAGTGCAGGTCTCCAACA 967

|||||
Db 616 TCACCGTCTCCACGAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAACA 675
QY 968 AAGCCCTCCAGCCCGCCATCGAGAAACCATCTCCAAAGCCAAAGGCGCAGCCCGAGAAC 1027
Db 676 AAGCCCTCCAGCCCGCCATCGAGAAACCATCTCCAAAGCCAAAGGCGCAGCCCGAGAA 735
QY 1028 CACAGGTGTACACCTGTCGCCCGCCATCCGGGATGAGTGCACCAAGACCAAGGTGAGCTGA 1087
Db 736 CACAGGTGTACACCTGTCGCCCGCCATCCGGGATGAGTGCACCAAGAA-CAGGTCAAGCTGA 794
QY 1088 CTGCGCTGTGTCAAAGGCTTCTATCCAGGACATCCCGTGGAGTGGGAGAGCAATGGGC 1147
Db 795 CTGCGCTGTGTCAAAGGCTTCTATCCAGGACATCCCGTGGAGTGGGAGAGCCATGGGC 854
QY 1148 AG-CCGGAGAACACTACAGACCCGCTCCCGTG---CTGGACTCCGACGCG-TCCTT 1202
Db 855 AGCCCGGAGAACACTACAGACCCGCTCCCGTGCTGGAACTCCGACGCTTCCCTT 914
QY 1203 CTTCCTCTACAGCAAGCTCACCTGGGACAGACGAGTGGCAGCA 1247
Db 915 CTTCCTCTACAGAAAGAGCTCCCGGGGGAACAAGCAGGTGGCA 959
RESULT 6
LOCUS BM007892 901 bp mRNA linear EST 30-OCT-2001
DEFINITION 603617577F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450611 5',
mRNA sequence.
ACCESSION BM007892
VERSION BM007892.1 GI:16522233
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 901)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1939 row: j column: 20
High quality sequence stop: 834.
Location/Qualifiers
1. .901
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5450611"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT 209 a 315 c 234 g 143 t
ORIGIN
Query Match 62.3%; Score 831.2; DB 13; Length 901;
Best Local Similarity 97.7%; Pred. No. 2.3e-190;
Matches 864; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

```
Qy 312 GGGCCAGGGAACACTAGTACCGCTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC 371
Db 19 GGGCCAGGAACCTGTGTACCGCTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCC 78
Qy 372 CTTGGGCAACCTCTCTCCAAAGACACCTCTCTGGGGGACAGCGGCCCTGGGTGCTGTCTAA 431
Db 79 CTTGGCAACCTCTCTCCAAAGACACCTCTCTGGGGGACAGCAGCCCTGGGTGCTGTCTAA 138
Qy 432 GGACTACTTCCCGCAACCGGTGACGGTGTCTGTAACCTACAGGCGCCTGACACGCGCGT 491
Db 139 GGACTACTTCCCGCAACCGGTGACGGTGTCTGTAACCTACAGGCGCCTGACACGCGCGT 198
Qy 492 GCACACCTTCCCGGCTCTCTACAGCTCTCAGGACTCTACTCCTCAGCAGCGTGTGAC 551
Db 199 GCACACCTTCCCGGCTCTCTACAGCTCTCAGGACTCTACTCCTCAGCAGCGTGTGAC 258
Qy 552 CGTCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAAGCTGAATCAAGGCCAG 611
Db 259 CGTCCCTCCAGCAGCTTGGGACCCAGACCTACATCTGCAAGCTGAATCAAGGCCAG 318
Qy 612 CAACCAAGGTGGACAAAGAGTGGAGCCCAATCTTGTGACAAACTCACACATGCC 671
Db 319 CAACCAAGGTGGACAAAGAGTGGAGCCCAATCTTGTGACAAACTCACACATGCC 378
Qy 672 ACCGTGCCCCAGCACTGAACTCGGGGGACCGCTCAGTCTTCTCTTCCCCCAAAACC 731
Db 379 ACCGTGCCCCAGCACTGAACTCGGGGGACCGCTCAGTCTTCTCTTCCCCCAAAACC 438
Qy 732 CAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGTGTGACGTGAG 791
Db 439 CAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGTGTGACGTGAG 498
Qy 792 CCACCAAGACCTCAGGTCAAGTTCAACTGTGAGCGCGCTGGAGTGCATATGC 851
Db 499 CCACCAAGACCTCAGGTCAAGTTCAACTGTGAGCGCGCTGGAGTGCATATGC 558
Qy 852 CAAGACAAAGCGCGGAGGAGCAGTACAACAGCAGTACCGTGTGTGACGCTCTCTAC 911
Db 559 CAAGACAAAGCGCGGAGGAGCAGTACAACAGCAGTACCGTGTGTGACGCTCTCTAC 618
Qy 912 CGTCTCAGCAGACCTGCGTGAATGCAAGGAGTACAAGTCAAGTCAAGTCTCCAACAAGC 971
Db 619 CGTCTCAGCAGACCTGCGTGAATGCAAGGAGTACAAGTCAAGTCTCCAACAAGC 678
Qy 972 CTTCCCAAGCCCATCGAGAAACCATCTCCAAAGCCAAAGGACGCGCCGAGAACCA 1031
Db 679 CTTCCCAAGCCCATCGAGAAACCATCTCCAAAGCC-AAGGACGCGCCGAGAACCA 737
Qy 1032 GGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGACCGGTGACCTGACCTG 1091
Db 738 GGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGACCGGTGACCTGACCTG 797
Qy 1092 CTTGGTCAAGAGCTTCTATCCAGCGACATCG-CCGTGGAGTGGGAGCAATGGGAGC 1150
Db 798 CTTGGTCAAGAGCTTCTATCCAGCGACATCGCCCGTGGAGTGGGAGGATCCGCGAGC 857
Qy 1151 CGGAGAACAACTACAAGACCAACGCTCCCGTGTGGACTCCGAC 1194
Db 858 CGGAGAACAACTACAAGACCAACGCTCCCGTGTGGACTCCGAC 901

RESULT 7
BQ708022
LOCUS BQ708022 918 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8353641 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279643
5', mRNA sequence.
ACCESSION BQ708022
VERSION BQ708022.1 GI:21846921
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE 1 (bases 1 to 918)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2469 row: 1 column: 20
High quality sequence stop: 667.
FEATURES
Location/Qualifiers
1..918
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 208 a 316 c 245 g 147 t 2 others
ORIGIN
Query Match 61.9%; Score 826.4; DB 14; Length 918;
Best Local Similarity 96.1%; Pred. No. 3.3e-189;
Matches 867; Conservative 0; Mismatches 33; Indels 2; Gaps 2;
Qy 309 CTGGGGCCAGGGAACACTAGTACCGCTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTT 368
Db 8 CTGGGGCCAGGGAACCGCTGTGTACCGCTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTT 67
Qy 369 CCCCTGTGCACCTCTCTCCAGAGCACCTCTGGGGGACAGCGCCCTGGGTGCTGCTGT 428
Db 68 CCCCTGTGCACCTCTCTCCAGAGCACCTCTGGGGGACAGCGCCCTGGGTGCTGCTGT 127
Qy 429 CAAGGACTACTTCCCGCAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTCACCAGCGG 488
Db 128 CAAGGACTACTTCCCGCAACCGGTGACGGTGTCTGGAACCTCAGCGCCCTCACCAGCGG 187
Qy 489 CGTGCACACCTTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGGAGGCTGT 548
Db 188 CGTGCACACCTTCCCGGCTGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGGAGGCTGT 247
Qy 549 GACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCAACAAGCC 608
Db 248 GACCGTGCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCAACAAGCC 307
Qy 609 CAGCAACACCAAGGTGGACAGAAAGTGGAGCCCAAAATCTTTGTGACAAACTCACAATG 668
Db 308 CAGCAACACCAAGGTGGACAGAAAGTGGAGCCCAAAATCTTTGTGACAAACTCACAATG 367
Qy 669 CCCACCGTCCCGCAGCACCTGAACTCGCGGGGACACCGTCACTCTTCTTCCCCCAAA 728
Db 368 CCCACCGTCCCGCAGCACCTGAACTCTTGGGGGACCGGTGAGTCTTCTTCCCCCAAA 427
Qy 729 ACCCAAGGACACCTCATGATCTCCCGGACCCCTCAGGTGCATCGTGGTGGTGGAGCT 788
Db 428 ACCCAAGGACACCTCATGATCTCCCGGACCCCTCAGGTGCATCGTGGTGGTGGAGCT 487
Qy 789 GAGCCACGAAGACCTCAGGTCAAGTTCAACTGGTACGTGGACGCGGTGGAGGTGCATAA 848
Db 488 GAGCCACGAAGACCTCAGGTCAAGTTCAACTGGTACGTGGACGCGGTGGAGGTGCATAA 547
```

```
QY 849 TGCCAAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGCAGTACCGTGTGGTTCAGCGTCCT 908
Db 548 TGCCAAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGCAGTACCGTGTGGTTCAGCGTCCT 607
QY 909 CACCGTCTGTGACACAGGAGTGGTGAATGGCAAGAGTACAAGTGAAGTCTCCACAA 968
Db 608 CACCGTCTGTGACACAGGAGTGGTGAATGGCAAGAGTACAAGTGAAGTCTCCACAA 667
QY 969 AGCCCTCCAGCCGCCCCATCTGAGAAACCATCTCAAAGCCAAAGGCGAGCCCGGAGAAC 1028
Db 668 AGCCCTCCAGCCGCCCCATCTGAGAAACCATCTCAAAGCCAAAGGCGAGCCCGGAGAAC 727
QY 1029 ACAGGTGTACACCTGTGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGTTCAGCCTGAC 1088
Db 728 ACAGGTGTACACCTGTGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGTTCAGCCTGGA 787
QY 1089 CTGCGTGTCAAAGCTTCTATCCAGCAGCATCGCCGT-GGAGTGGGAGAGCAATGGGC 1147
Db 788 CTGCGTGTCAAAGCTTCTATCCAGCAGCATCCCGGGGAGTGGGAGAGCAATGGGC 847
QY 1148 AG-CCGGAGAAACACTACAAGACCAACGCTCCCGTGTGGACTCCGAGCGCTCTCTTC 1206
Db 848 AGCCCGGAGAACACTACAAGACCAACGCTCCCGGGTGGGACTCCCGAGCGGTCTCTT 907
QY 1207 CT 1208
Db 908 CT 909

RESULT 8
BQ063185
LOCUS
DEFINITION BQ063185 1029 bp mRNA linear EST 02-APR-2002
5', mRNA sequence.
AGENCOURT_6876667 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924769
ACCESSION BQ063185
VERSION BQ063185.1 GI:19890681
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1029)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM2095 row: g column: 10
High quality sequence stop: 723.
Location/Qualifiers
1..1029
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5924769"
/clone_lib="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site: 1; XhoI; Site 2;
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
```

FEATURES

source

```
BASE COUNT 237 a 350 c 276 g 165 t 1 others
ORIGIN
Query Match 61.5%; Score 821.2; DB 14; Length 1029;
Best Local Similarity 98.7%; Pred. No. 6.3e-188;
Matches 859; Conservative 0; Mismatches 8; Indels 3; Gaps 3;
QY 387 CAAGAGCACCTCTGGGGGACAGCGCCCTGGCTGGTCAAGGACTACTTCCCGCA 446
Db 4 CCAGAGCACCTCTGGGGGACAGCGCCCTGGCTGGTCAAGGACTACTTCCCGCA 63
QY 447 ACCGGTACGGTGTCTGGAACTCAGGCGCCCTGACAGCGGCGTGCACACCTTCCCGG 506
Db 64 ACCGGTACGGTGTCTGGAACTCAGGCGCCCTGACAGCGGCGTGCACACCTTCCCGG 123
QY 507 TGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTTCAGCAG 566
Db 124 TGTCTTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGCCTTCAGCAG 183
QY 567 CTTGGGCACCCAGACCTTACATCTGCAACGTGAATCAAGCCCGCAGCAACACCAAGTGA 626
Db 184 CTTGGGCACCCAGACCTTACATCTGCAACGTGAATCAAGCCCGCAGCAACACCAAGTGA 243
QY 627 CAAGAAAGTGGAGCCCAAAATCTTTGTGACAAATCAACATGCCACCGTGCACACACC 686
Db 244 CAAGAAAGTGGAGCCCAAAATCTTTGTGACAAATCAACATGCCACCGTGCACACACC 303
QY 687 TGAACCTCGCGGGGCGACCGTCACTCTCTCTTCCCGCCCAAAACCAAGGACACCTCAT 746
Db 304 TGAACCTCGCGGGGCGACCGTCACTCTCTCTTCCCGCCCAAAACCAAGGACACCTCAT 363
QY 747 GATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 806
Db 364 GATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 423
QY 807 GGTCAAGTTCACTGGTGTGAGCGGTGAGCGGTGAGAGTGATATGCGCAAGCAAGCGCG 866
Db 424 GGTCAAGTTCACTGGTGTGAGCGGTGAGCGGTGAGAGTGATATGCGCAAGCAAGCGCG 483
QY 867 GGAGGACAGTACAACAGCAGTACCGTGGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 926
Db 484 GGAGGACAGTACAACAGCAGTACCGTGGTGGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 543
QY 927 CTGGCTGAATGGCAAGGAGTACAAGTGAAGTGAAGTCTCCAACAAAGCCCTCCAGCC 986
Db 544 CTGGCTGAATGGCAAGGAGTACAAGTGAAGTGAAGTCTCCAACAAAGCCCTCCAGCC 603
QY 987 CGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGACACAGGTGTACACCTGCC 1046
Db 604 CGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGACACAGGTGTACACCTGCC 663
QY 1047 CCCATCCCGGATGAGTGAACCAAGACAGGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1106
Db 664 CCCATCCCGGATGAGTGAACCAAGACAGGTGAACCAAGTCAAGTCAAGTCAAGTCAAG 723
QY 1107 CTATCCAGCAGCATCCCGTGGAGTGGAGAGCAATGGGAGCGGAGCAACAACTACAA 1166
Db 724 CTATCCAGCAGCATCCCGTGGAGTGGAGAGCAATGGGAGCGGAGCAACAACTACAA 783
QY 1167 GACCAACCCCT-CCCGTGTCTGGACTCCGACCGGTCTCTTCTCTCTTCTCTCTCTCT 1224
Db 784 GACCAACCCCTCCCGGTGTCTGGACTCCGACCGGTCTCTTCTCTCTCTCTCTCTCTCT 843
QY 1225 GTGGACAGAGCA-GGTGGCAGCAGGGGAA 1253
Db 844 GTGGACAGAGCAGGGTGGCAGCAGGGGGA 873

RESULT 9
BQ711255
LOCUS
DEFINITION BQ711255 887 bp mRNA linear EST 16-JUL-2002
AGENCOURT_8443471 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281659
5', mRNA sequence.
```

[illegible]

BASE COUNT	241 a	330 c	259 g	165 t	
ORIGIN	NIH_MGC Library."				
Query Match	61.4%; Score 819.6; DB 14; Length 995;				
Best Local Similarity	97.1%; Pred. No. 1.5e-187;				
Matches 856; Conservative	0; Mismatches 24; Indels 2; Gaps 2;				
QY	307	GACTGGGGCCAGGGAACACTAGTACACGCTCTCTCTCAGCCTCCACCAAGGCGCCATCGGTC	366		
Db	16	GATTGGGGCCAGGGAACGCTGTCACGCTCTCTCTCAGCCTCCACCAAGGCGCCATCGGTC	75		
QY	367	TTCCCCCTGGCACCCCTCTCTCAAGAGACACTCTCTGGGGGCACAGGGCCCTGGGCTGCCG	426		
Db	76	TTCCCCCTGGCACCCCTCTCTCAAGAGACACTCTCTGGGGGCACAGGGCCCTGGGCTGCCG	135		
QY	427	GTCAAGGACTACTTCCCGGAACCGGTGACGGTGCCTGGAACCTCAGCGCCCTGACCCAGC	486		
Db	136	GTCAAGGACTACTTCCCGGAACCGGTGACGGTGCCTGGAACCTCAGCGCCCTGACCCAGC	195		
QY	487	GGCGTGCACACACTTCCCGGCTGTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTG	546		
Db	196	GGCGTGCACACACTTCCCGGCTGTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTG	255		
QY	547	GTGACCGTGCCCTTCAGCAGACTTGGGCACCAGACCTTACATCTGCAACGTGAATCAACAG	606		
Db	256	GTGACCGTGCCCTTCAGCAGACTTGGGCACCAGACCTTACATCTGCAACGTGAATCAACAG	315		
QY	607	CCGAGCAACACAAAGTGGACAAGAAAGTGGAGCCCAAACTTTGTGACAAAATCACACA	666		
Db	316	CCGAGCAACACAAAGTGGACAAGAAAGTGGAGCCCAAACTTTGTGACAAAATCACACA	375		
QY	667	TGCCCAACCGTGCCCAAGCACTGAACCTCGGGGGGACCGCTCAGTCTTCTCTTCCGCCCA	726		
Db	376	TGCCCAACCGTGCCCAAGCACTGAACCTCGGGGGGACCGCTCAGTCTTCTCTTCCGCCCA	435		
QY	727	AAACCCAAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTCAACATCGGTGGTGGTGGAC	786		
Db	436	AAACCCAAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTCAACATCGGTGGTGGTGGAC	495		
QY	787	GTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAT	846		
Db	496	GTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAT	555		
QY	847	AATGCCAAAGCAAAAGCCGGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTTCACGCTC	906		
Db	556	AATGCCAAAGCAAAAGCCGGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTTCACGCTC	615		
QY	907	CTCACGGTCTGCACACGAGACTTGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCTCCAAC	966		
Db	616	CTCACGGTCTGCACACGAGACTTGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCTCCAAC	675		
QY	967	AAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGACGCCCGAGAA	1026		
Db	676	AAAGCCCTCCAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGACGCCCGAGAA	735		
QY	1027	CCACAGGTGTACACCTTGCCCCCATCCCGGGATGAGCTGACCAAGAACACAGGTTCAGCCCTG	1086		
Db	736	CCACAGGTGTACACCTTGCCCCCATCCCGGGATGAGCTGACCAAGAACACAGGTTCAGCCCTG	795		
QY	1087	ACCTGCTGGTCAAAAGGCTTCTATCCAGCGACATCCCGCTGGAGTGGG-AGAGCAATGG	1145		
Db	796	ACCTGCTGGTCAAAAGGCTTCTATCCAGCGACTTCTCCCGCTGGAGTGGGAAAGCAATGG	855		
QY	1146	GCAGCCGGAGAACAACTACAGAA-CCAGCCCTCCCGTGCTGG	1186		
Db	856	GAAGCCGGAAAAAATACTAAGACCCCGCCTCCCGTCTTG	897		
RESULT 11					
BQ711291					
LOCUS	BQ711291				
DEFINITION	AGENCOURT_8347186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279096				
	linear EST 16-JUL-2002				

```

5', mRNA sequence.
BQ711291
VERSION
BQ711291.1 GI:21850190
EST.
KEYWORDS
human.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 881)
N1H-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2468 row: c column: 01
High quality sequence stop: 721.
Location/Qualifiers
1. .881
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6279096"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 220 a 285 c 237 g 139 t
ORIGIN

Query Match 60.3%; Score 805.6; DB 14; Length 881;
Best Local Similarity 99.5%; Pred. No. 3.5e-184;
Matches 808; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY	516	GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC	575
Db	1	GTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC	60
QY	576	CCAGACCTACATCTGCACCAAGTGAATCAACAGCCGAGCAACACCAAGGTGGACAGAAAGT	635
Db	61	CCAGACCTACATCTGCACCAAGTGAATCAACAGCCGAGCAACACCAAGGTGGACAGAAAGT	120
QY	636	GGAGCCCAAAATCTTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCGC	695
Db	121	TGAGCCCAAAATCTTTGTGACAAAACCTCACACATGCCACCGTGCCAGCACCTGAACTCGT	180
QY	696	GGGGGACCGGTACGTCTTCCTTTCCCGCCCAAAACCCAAAGACACCCCTCATGATCTCCCG	755
Db	181	GGGGGACCGGTACGTCTTCCTTTCCCGCCCAAAACCCAAAGACACCCCTCATGATCTCCCG	240
QY	756	GACCCCTGAGGTGCACATGCGTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTCAAGTT	815
Db	241	GACCCCTGAGGTGCACATGCGTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTCAAGTT	300
QY	816	CAACTGTGTACGTGGACGCGGTGGAGGTGCATAATGCCAAAGCCCGCGGAGGAGCA	875
Db	301	CAACTGTGTACGTGGACGCGGTGGAGGTGCATAATGCCAAAGCCCGCGGAGGAGCA	360
QY	876	GTACAACAGCACGTACCGTGTGGTACGGTCTCTACACCGTCTCTGCACCCAGGACTGGCTGAA	935
Db	361	GTACAACAGCACGTACCGTGTGGTACGGTCTCTACACCGTCTCTGCACCCAGGACTGGCTGAA	420

RESULT	11
BQ711291	
LOCUS	BQ711291
DEFINITION	AGENCOURT_8347186 NIH MGC clone Homo sapiens cDNA clone IMAGE:6279096
	linear mRNA 881 bp EST 16-JUL-2002


```

ACCESSION BQ7111727
VERSION BQ7111727.1 GI:21850626
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 936)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2518 row: k column: 18
High quality sequence stop: 547.
FEATURES
source
Location/Qualifiers
1..936
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 231 a 306 c 245 g 152 t 2 others
ORIGIN
Query Match 59.5%; Score 794.2; DB 14; Length 936;
Best Local Similarity 98.1%; Pred. No. 2.1e-181;
Matches 824; Conservative 0; Mismatches 14; Indels 2; Gaps 2;
QY 497 CCTTCCCGGCTGCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGC 556
DB 10 CCTTCCCGGCTGCTCCTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTACCGTGC 69
QY 557 CCTCCAGCAGCTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCGCAGCA 616
DB 70 CCTCCAGCAGCTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCGCAGCA 129
QY 617 CCAAGGTGGACAGAAGAGTGGAGCCCAATCTTGTGACAAAATCACAATGCCACCGT 676
DB 130 CCAAGGTGGACAGAAGAGTGGAGCCCAATCTTGTGACAAAATCACAATGCCACCGT 189
QY 677 GCCCAGCAGCTGACCTGCGGGGGGACCGTCACTCTCTCTCCCGCCCAAAACCCAAAG 736
DB 190 GCCCAGCAGCTGACCTGCGGGGGGACCGTCACTCTCTCTCTCCCGCCCAAAACCCAAAG 249
QY 737 ACACCTTCATGATCTCCCGGACCCCTCAGGTACATCGCTGGTGGAGCTGAGCCACG 796
DB 250 ACACCTTCATGATCTCCCGGACCCCTCAGGTACATCGCTGGTGGAGCTGAGCCACG 309
QY 797 AAGACCTGAGGTCAAGTTCACTGTPACGTGGACCGCGTGGAGGTGCATAATGCCAAGA 856
DB 310 AAGACCTGAGGTCAAGTTCACTGTPACGTGGACCGCGTGGAGGTGCATAATGCCAAGA 369
QY 857 CAAGCCGCGGGAGGACAGTACACAGCAGTACCGTGTGCTCAGCGTCTCACCGTCC 916
DB 370 CAAGCCGCGGGAGGACAGTACACAGCAGTACCGTGTGCTCAGCGTCTCACCGTCC 429
QY 917 TGCACAGGAGTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCACAACAAAGCCCTCC 976

Db 430 TGCACAGGAGTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCACAACAAAGCCCTCC 489
QY 977 CAGCCCCCATCGAAGAAACCATCTCCAAAGCCAAAGGCGCAGCCCGGAGAACCAACAGTGT 1036
Db 490 CAGCCCCCATCGAAGAAACCATCTCCAAAGCCAAAGGCGCAGCCCGGAGAACCAACAGTGT 549
QY 1037 ACACCTGCCCGGATCCCGGGATGAGTGCACCAAGAACCAAGTGCAGCTGACCTGCCTGG 1096
Db 550 ACACCTGCCCGGATCCCGGGATGAGTGCACCAAGAACCAAGTGCAGCTGACCTGCCTGG 609
QY 1097 TCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGCGAGCCGAGGA 1156
Db 610 TCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGCGAGCCGAGGA 669
QY 1157 ACAACTACAAGACA-CGCTCCCGTGTGCTGAGCTCCGAGGCTCTTCTTCTCTACAGC 1215
Db 670 ACAACTAGNAGAACCACCGCTCCGCTGCTGAGCTCCGAGCTCTTCTTCTCTACAGC 729
QY 1216 AAGCTCACCGTGGACAAGCAGGAGTGGCAGCAGGGGAAACGCTTCTCATGCTCCGTGATG 1275
Db 730 AAGCTCACCGTGGACAAGCAGGAGTGGCAGCAGGGGAAACGCTTCTCATGCTCCGGATG 789
QY 1276 CATGAGGCTCTGCACAACCACTACACGAGAGAGCCCTCTCCCTGTCTCCGGTAAATGA 1335
Db 790 CATGAGGCTCTGCAC-ACCACCTAACCGCAGAGAGCCCTCTTCTCTCTCCCGGAAATGA 848

RESULT 14
LOCUS BQ705928 940 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_7976186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214795
5', mRNA sequence.
ACCESSION BQ705928
VERSION BQ705928.1 GI:21844827
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 940)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2382 row: k column: 20
High quality sequence stop: 619.
FEATURES
Location/Qualifiers
1..940
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6214795"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 235 a 318 c 240 g 147 t
ORIGIN

```

Query Match	59.4%	Score 792.8	DB 14	Length 940
Best Local Similarity	99.0%	Prod. No. 4.5e-181		
Matches 808	Conservative	0	Mismatches 7	Indels 1
Qy 521	CAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGA	580		
Db 1	CAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGA	60		
Qy 581	CCTACATCTGCAACGTGTAATCAACAGCCAGCAACCAAGGTGGACAAAGTGGAGC	640		
Db 61	CCTACATCTGCAACGTGTAATCAACAGCCAGCAACCAAGGTGGACAAAGTGGAGC	120		
Qy 641	CCAATCTTGTGACAAAACTCACACATGCCACCGTGCCAGCAGCTGAACCTCGCGGGG	700		
Db 121	CCAATCTTGTGACAAAACTCACACATGCCACCGTGCCAGCAGCTGAACCTCGCGGGG	180		
Qy 701	CACCGTCAGTCTTCTCTTCCCTCCCAACCCAAAGGACACCTCATGATCTCCCGAGCC	760		
Db 181	GACCGTCAGTCTTCTCTTCCCTCCCAACCCAAAGGACACCTCATGATCTCCCGAGCC	240		
Qy 761	CTGAGGTCACATCGTGGTGGTGACGTGACCCAGCAGAGCCCTCAGGTCAGTTCACT	820		
Db 241	CTGAGGTCACATCGTGGTGGTGACGTGACCCAGCAGAGCCCTCAGGTCAGTTCACT	300		
Qy 821	GGTAGTGGACGGGTGGAGGTGCATAATGCCAAGCAAAAGCCGGGAGGAGCAGTACA	880		
Db 301	GGTAGTGGACGGGTGGAGGTGCATAATGCCAAGCAAAAGCCGGGAGGAGCAGTACA	360		
Qy 881	ACAGCAGTACCGTGGTGTACAGCTCTCACCGTCTGCACAGGACTGGGTGAATGGCA	940		
Db 361	ACAGCAGTACCGTGGTGTACAGCTCTCACCGTCTGCACAGGACTGGGTGAATGGCA	420		
Qy 941	AGGAGTACAAGTGAAGGTCCTCCAACAAAGCCCTCCAGCCGCCATCCAGAAAAACCATCT	1000		
Db 421	AGGAGTACAAGTGAAGGTCCTCCAACAAAGCCCTCCAGCCGCCATCCAGAAAAACCATCT	480		
Qy 1001	CCAAGCCAAAGGGAGGCCCGGAGAACACAGGTGTATACCCCTGCCCCCATCCCGGGATG	1060		
Db 481	CCAAGCCAAAGGGAGGCCCGGAGAACACAGGTGTATACCCCTGCCCCCATCCCGGGATG	540		
Qy 1061	AGCTGACCAAGAACCCAGGTGACGCTGACCTGCCTGGTCAAAAGGCTTCATCCACAGCGACA	1120		
Db 541	AGCTGACCAAGAACCCAGGTGACGCTGACCTGCCTGGTCAAAAGGCTTCATCCACAGCGACA	600		
Qy 1121	TCGCGGTGGAGTGGAGAGCAATGGCGAGCCGGAGAACACTACAAGACCACGCTCCCG	1180		
Db 601	TCGCGGTGGAGTGGAGAGCAATGGCGAGCCGGAGAACACTACAAGACCACGCTCCCG	660		
Qy 1181	TGCTGGACTCCGAGCGGCTCTTCTTCTCTACGCAAGCTCACCGTGCACAGAGCAGGT	1240		
Db 661	TGCTGGACTCCGAGCGGCTCTTCTTCTCTACGCAAGCTCACCGTGCACAGAGCAGGT	720		
Qy 1241	GGCAGCAGGGGAAGCTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAACACTACA	1300		
Db 721	GGCAGCAGGGGAAGCTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAAACACTACA	780		
Qy 1301	CGC-AGAAAGACCTCTCCCTGCTCCGGGTAAATGA	1335		
Db 781	CGCAAAAGACCTCTCCCTGCTCCGGGTAAATGA	816		

RESULT 15	BM9114504	ACCESSION	BM9114504	980 bp	linear	EST 12-MAR-2002
LOCUS	BM9114504	DEFINITION	ACCESSION	NIH_MGC_113	cdna clone	IMAGE:5480185
			5', mRNA sequence.			
		ACCESSION	BM9114504			
		VERSION	BM9114504.1	GI:19364883		
		KEYWORDS	EST.			
		SOURCE	human.			
		ORGANISM	human sapiens			
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			

REFERENCE	1 (bases 1 to 980)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Mark Watson cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LICM2002 row: k column: 02 High quality sequence stop: 689.

FEATURES
SOURCE

```

location/qualifiers
1. .980
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5480185"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: spleen; Vector: pOTB7; Site:1; XhoI: Site:2;
EcORI: cDNA made by oligo-dT priming. Directionally cloned
into EcORI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
235 a 332 c 155 t 2 others
BASE COUNT
ORIGIN

```

BASE COUNT
ORIGIN

Query Match	59.0%	Score 788;	DB 14;	Length 980;
Best Local Similarity	97.1%	Pred. No. 6.7e-180;		
Matches 824; Conservative	0;	Mismatches 21;	Indels 4;	Gaps 2;

Qy	335	TCTCCTCAGCCTCACCAGGGCCCATCGGTCTTCCGCCCTGGCACCCCTCTCTCCAGAGCA	394
Db	1	TCTCCTCAGCCTCACCAGGGCCCATCGGTCTTCCGCCCTGGCACCCCTCTCTCCAGAGCA	60
Qy	395	CCTCTGGGGGCACAGCGGCCCTGGGCTGCCGTGTCGAAGGACTACTTCCCCGAACCGGTGA	454
Db	61	CCTCTGGGGGCACAGCGGCCCTGGGCTGCCGTGTCGAAGGACTACTTCCCCGAACCGGTGA	120
Qy	455	CGGTGTGCGTGAACCTCAGGCGCCCTGACCAGCGGGGTGCACACCTTCCGGGCTGTCTTAC	514
Db	121	CGGTGTGCGTGAACCTCAGGCGCCCTGACCAGCGGGGTGCACACCTTCCGGGCTGTCTTAC	180
Qy	515	AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCTCCAGCAGCTTGGGCA	574
Db	181	AGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTCTCCAGCAGCTTGGGCA	240
Qy	575	CCCAGACCTACATCTGCAACGTGAATCACAAAGCCCAACACCAAGGTGGACAAAG	634
Db	241	CCCAGACCTACATCTGCAACGTGAATCACAAAGCCCAACACCAAGGTGGACAAAG	300
Qy	635	TGGAGCCCAATCTGTGACAAAACCTCACACATGCCACCGTGCCAGCAGCCTCAACTCG	694
Db	301	TTGAGCCCAATCTGTGACAAAACCTCACACATGCCACCGTGCCAGCAGCCTCAACTCC	360
Qy	695	CGGGGACCGCTCAGTCTTCTCTTCCCCCCAAACCCAAAGGACACCCCTCATGATCTCCC	754
Db	361	TGGGGGACCGCTCAGTCTTCTCTTCCCCCCAAACCCAAAGGACACCCCTCATGATCTCCC	420
Qy	755	GGACCCCTG-AGGTCACATCGGTGGTGGACGTGAGCCAGACACCTTGAGGTCAG	813
Db	421	GGACCCCTGAGGTCACATCGGTGGTGGTGGACGTGAGCCAGACACCTTGAGGTCAG	480
Qy	814	TTCAACTCGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCGGGAGG	873
Db	481	TTCAACTCGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCGGGAGG	540

Qy	874	CAGTACAA	CAGCAGCTACCGTGTGGTTCAGCTCTCA	CCGCTCTGCACGAGCACTGGCTG	933
Db	541	CAGTACAA	CAGCAGCTACCGTGTGGTTCAGCTCTCA	CCGCTCTGCACGAGCACTGGCTG	600
Qy	934	AATGGCA	AGGAGTACAAGTGCAAGTGCTCCAA	AAAGCCCTCCAGACGCCCATCGAGAAA	993
Db	601	AATGGCA	AGGAGTACAAGTGCAAGTGCTCCAA	AAAGCCCTCCAGACGCCCATCGAGAAA	660
Qy	994	ACCATCT	CCAAAGCCAAAGGGCAGCCCGAGAA	ACACAGGTGTATACCCCTGCCCCCATCC	1053
Db	661	ACCATCT	CCAAAGCCAAAGGGCAGCCCGAGAA	ACACAGGTGTATACCCCTGCCCCCATCC	720
Qy	1054	CGGGAT	CAGCTGACCAAGAACCAGGTTCAGCCT	TGACCTGCCTGGTCTCAAGGGTCTTATCCC	1113
Db	721	CGGGAT	CAGCTGACCAAGAACCAGGTTCAGCCT	TGACCTGCCTGGTCTCAAGGGTCTTATCCC	780
Qy	1114	AGCGACAT	CGCCGTGGAGTGGG--AGAGCAAT	GGCAGCCGGGAGAACAACTACAAGACC	1170
Db	781	ANCGACAT	CGCCGTGGAGGGGAA	AAACAAAGGGCGACCCGAGAACAACTACAAGACC	840
Qy	1171	ACGCCT	CTCC	1179	
Db	841	CCGCCCT	CTCC	849	

Search completed: April 26, 2003, 07:27:01
Job time : 1780.31 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:50:01 ; Search time 268.58 Seconds
(without alignments)
11193.756 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 1335

Sequence: 1 gaggtgcagctgggtggagtc.....ccctgtctccgggtaaatga 1335

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

1:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20:	/SID22/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1335	100.0	1335	21	AAZ34748 Humanised anti-CD2
2	1149.2	86.1	1442	22	AAZ34748 Plasmid Glambda-1B
3	1147.8	86.0	1798	21	AAZ34748 Human colon cancer
4	1147.2	85.9	1437	19	AAZ35487 Macaque primatized
5	1147.2	85.9	1437	24	AAZ17245 DNA sequence of a
6	1145.6	85.8	1437	18	AAT13847 Primatized anti-hu
7	1145	85.8	1616	24	AAZ562785 cDNA sequence #572
8	1143.6	85.7	1576	14	AAQ49944 Human anti-HBs hea
9	1142.8	85.6	1386	14	AAQ49834 Anti-HIV-1 recomb

10	1142.8	85.6	6291	22	AAZ34748	Plasmid Glambda-1A
11	1142.2	85.6	19035	19	AAZ34748	Traget plasmid Man
12	1141.8	85.5	1427	19	AAZ34748	Plasmid Hu19HCpcd
13	1141.8	85.5	1427	19	AAZ34748	Plasmid Hu19HCpcd
14	1140.2	85.4	1427	19	AAZ34748	Plasmid Hu19HCpcd
15	1136.6	85.1	1617	24	AAZ34748	Plasmid Hu19HCpcd
16	1136	85.1	1430	24	AAZ34748	cDNA sequence #571
17	1135	85.0	1347	21	AAZ34748	cDNA of the heavy
18	1133.8	84.9	7521	22	AAZ34748	cDNA encoding a ra
19	1131	84.7	1356	22	AAZ34748	Bicistronic chimera
20	1128.8	84.6	6284	19	AAZ34748	Human recombinant
21	1125.8	84.3	1641	15	AAZ34748	Plasmid Hu19HCpcd
22	1121.4	84.0	9182	24	AAZ34748	chir84.12 H3 heavy
23	1121.2	84.0	1644	22	AAZ34748	Baculovirus expres
24	1119.8	83.9	9182	24	AAZ34748	Human cDNA encodin
25	1118.6	83.8	1549	13	AAZ34748	Plasmid pTRABac/9F
26	1117	83.7	1412	13	AAZ34748	Encodes heavy chai
27	1105.2	82.8	1598	24	AAZ34748	Sequence of the ch
28	1104.8	82.8	1404	22	AAZ34748	Human cDNA encodin
29	1102.2	82.6	2196	22	AAZ34748	Humanised HMFGL he
30	1102.2	82.6	2226	22	AAZ34748	Humanised HMFGL h
31	1100	82.4	1590	24	AAZ34748	Human cDNA encodin
32	1096.6	82.1	2190	22	AAZ34748	Humanised HMFGL h
33	1096.6	82.1	2220	22	AAZ34748	Humanised HMFGL h
34	1095.8	82.1	2193	22	AAZ34748	Humanised HMFGL h
35	1095.8	82.1	2223	22	AAZ34748	Humanised HMFGL h
36	1089	81.6	2974	22	AAZ34748	Humanised HMFGL h
37	1082.6	81.1	8119	20	AAZ34748	Synthetic EST-deri
38	1082.6	81.1	8119	21	AAZ34748	Plasmid pG4V11N35
39	1082.6	81.1	8120	21	AAZ34748	Nucleotide sequenc
40	1082	81.0	4207	24	AAZ34748	Humanised anti-IL-
41	1082	81.0	4207	24	AAZ34748	Cytomegalovirus (C
42	1082	81.0	5732	24	AAZ34748	Cytomegalovirus (C
43	1082	81.0	5732	24	AAZ34748	Mouse mammary tumo
44	1082	81.0	9183	24	AAZ34748	Mouse mammary tumo
45	1082	81.0	9183	24	AAZ34748	Alpha-lactalbumin

ALIGNMENTS

RESULT 1
AAZ34748
ID AAZ34748 standard; cDNA; 1335 bp.
XX AC AAZ34748;
XX AC AAZ34748;
DT 15-FEB-2000 (first entry)
XX DE Humanised anti-CD23 Mab C11 heavy chain cDNA.
XX KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse; human;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes;
KW B-cell malignancy; therapy; ds.
XX OS Homo sapiens.
OS Synthetic.
XX WO9958679-A1.
XX PN WO9958679-A1.
XX PD Human colon cancer
XX PD Macaque primatized
XX PF DNA sequence of a
XX PF Primatized anti-hu
XX PF cDNA sequence #572
XX PR Human anti-HBs hea
XX PR Anti-HIV-1 recomb

PA (GLAX) GLAXO GROUP LTD.
XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
PI WPI; 2000-053101/04.
XX P-PSDB; AAY32263.
DR
PT Cell receptor specific antibodies useful for treating e.g. arthritis,
XX diabetes, multiple sclerosis and psoriasis -
XX Claim 17: Fig 4; 81pp; English.
XX
XX This DNA sequence encodes the heavy chain of humanised anti-CD23
CC (IgE receptor, FCER1) monoclonal antibody C11, composed of a human
CC framework (HSIGKVII) and the heavy chain complementarity determining
CC regions (see AAY32256-58) of murine antibody C11. The invention
CC provides altered antibodies, such as chimeric or humanised
CC antibodies, which comprise sufficient of the amino acid sequences
CC of the C11 light and heavy chain complementarity determining regions
CC to render them capable of binding to the CD23 type II molecule
CC expressed on haematopoietic cells. The antibodies are used to block
CC soluble CD23 formation in human therapy, for the treatment of
CC arthritis, lupus erythematosus, Hashimoto's thyroiditis, multiple
CC sclerosis, diabetes, uveitis, dermatitis, psoriasis, urticaria,
CC nephrotic syndrome, glomerulonephritis, inflammatory bowel disease,
CC ulcerative colitis, Crohn's disease, Sjogren's syndrome, allergies,
CC allergic asthma, intrinsic asthma, acute asthmatic exacerbation,
CC rhinitis, eczema, graft-versus-host disease, COPD, insulinitis,
CC bronchitis (particularly chronic bronchitis) or diabetes
CC (particularly type 1 diabetes), and B-cell malignancies (claimed).
CC They are also useful for studying interactions between CD23 and
CC various ligands and determining the binding agents.
XX
XX Sequence 1335 BP; 321 A; 414 C; 360 G; 240 T; 0 other;

Query Match 100.0%; Score 1335; DB 21; Length 1335;
Best Local Similarity 100.0%; Pred. No. 3.1e-251; Indels 0; Gaps 0;
Matches 1335; Conservative 0; Mismatches 0;

Qy 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTC 60
Db 1 GAGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTC 60

Qy 61 TCCTGTGAGCTAGCGGATTCACCTTTTCAGTGGCTACTGGATGCTGGTCCGGCCAGGCT 120
Db 61 TCCTGTGAGCTAGCGGATTCACCTTTTCAGTGGCTACTGGATGCTGGTCCGGCCAGGCT 120

Qy 121 CCAGGGAAGGGCTCGAGTGGGTTGCTGAATTAGATTGAATCTGATAATTATGCAACA 180
Db 121 CCAGGGAAGGGCTCGAGTGGGTTGCTGAATTAGATTGAATCTGATAATTATGCAACA 180

Qy 181 CATTATCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
Db 181 CATTATCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240

Qy 241 CTGTATCTGCAATTAACAGCCTTGAACCCGAGGACACAGCCGTTACTGTACAGAT 300
Db 241 CTGTATCTGCAATTAACAGCCTTGAACCCGAGGACACAGCCGTTACTGTACAGAT 300

Qy 301 TTCTATAGCTGGGGCCAGGAACTAGTCCACCTCTCCTCAGCTCCACCAAGGGGCCA 360
Db 301 TTCTATAGCTGGGGCCAGGAACTAGTCCACCTCTCCTCAGCTCCACCAAGGGGCCA 360

Qy 361 TCGGTCTTCCCTCGGCACCTCTCCAAAGAGCACCTCTGGGGGCACAGGGCCCTGGGC 420
Db 361 TCGGTCTTCCCTCGGCACCTCTCCAAAGAGCACCTCTGGGGGCACAGGGCCCTGGGC 420

Qy 421 TGCTGTGTCAGGACTACTTCCCGGAACCGGTGACGGTGTCTGCGAACTCAGGCGCCCTG 480
Db 421 TGCTGTGTCAGGACTACTTCCCGGAACCGGTGACGGTGTCTGCGAACTCAGGCGCCCTG 480

Qy 481 ACCAGCGGCTGCACACCTTCCCGGCTGTCTCTACAGCTCCTCAGGACTCTACTCCCTCAGC 540
Db 481 ACCAGCGGCTGCACACCTTCCCGGCTGTCTCTACAGCTCCTCAGGACTCTACTCCCTCAGC 540

Db 481 ACCAGCGGCTGCACACCTTCCCGGCTGTCTCTACAGCTCCTCAGGACTCTACTCCCTCAGC 540
Qy 541 AGCGTGGTGACCGTGCCTTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAGGTGAAT 600
Db 541 AGCGTGGTGACCGTGCCTTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAAGGTGAAT 600
Qy 601 CACAAGCCCGAGCAACACCAAGGTGGACAAGAGTGGAGCCCAAAATCTTGTGACAAAAC 660
Db 601 CACAAGCCCGAGCAACACCAAGGTGGACAAGAGTGGAGCCCAAAATCTTGTGACAAAAC 660
Qy 661 CACACATGCCACCGTGGCCAGCACCTGAATCGCGGGGGACCGTCACTTCTCTCTTC 720
Db 661 CACACATGCCACCGTGGCCAGCACCTGAATCGCGGGGGACCGTCACTTCTCTCTTC 720
Qy 721 CCCCCAAAACCCCAAGACACACCTCATGATCTCCCGGACCCCTGAGGTACATCGCTGGTG 780
Db 721 CCCCCAAAACCCCAAGACACACCTCATGATCTCCCGGACCCCTGAGGTACATCGCTGGTG 780
Qy 781 GTGGAGCTGAGCCACGAAGACCCCTGAGGTCAAAGTTCAACTGTGTAGTGGACGGCTGGAG 840
Db 781 GTGGAGCTGAGCCACGAAGACCCCTGAGGTCAAAGTTCAACTGTGTAGTGGACGGCTGGAG 840
Qy 841 GTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACCTACCGTGTGCTC 900
Db 841 GTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCACCTACCGTGTGCTC 900
Qy 901 AGCGTCTCTCACCGTCTGCAACAGGACTGGCTGAATGCGAAGGAGTACAAGTGCAGGTG 960
Db 901 AGCGTCTCTCACCGTCTGCAACAGGACTGGCTGAATGCGAAGGAGTACAAGTGCAGGTG 960
Qy 961 TCCAAACAAGCCCTCCACGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCC 1020
Db 961 TCCAAACAAGCCCTCCACGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCC 1020
Qy 1021 CGAAGAACACAGGTGTACACCTGCCCCCATCCCGGGATGAGTGCACCAAGAACAGGTG 1080
Db 1021 CGAAGAACACAGGTGTACACCTGCCCCCATCCCGGGATGAGTGCACCAAGAACAGGTG 1080
Qy 1081 AGCGTACCTGCTGGTCAAAGCTTCTATCCAGGACATCGCGTGGAGTGGAGGAGG 1140
Db 1081 AGCGTACCTGCTGGTCAAAGCTTCTATCCAGGACATCGCGTGGAGTGGAGGAGG 1140
Qy 1141 AATGGCAGCCGAGAAACAACACTACAAGACACCGCTCCCGTGTCTGGACTCCCGACGGCTCC 1200
Db 1141 AATGGCAGCCGAGAAACAACACTACAAGACACCGCTCCCGTGTCTGGACTCCCGACGGCTCC 1200
Qy 1201 TTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGAGAGTGGCAGGAGGGAACGTCTTC 1260
Db 1201 TTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGAGAGTGGCAGGAGGGAACGTCTTC 1260
Qy 1261 TCATGCTCGTGATGATGAGGTCTGACACCACTACACCGCAGAAAGCCCTCTCCCTG 1320
Db 1261 TCATGCTCGTGATGATGAGGTCTGACACCACTACACCGCAGAAAGCCCTCTCCCTG 1320
Qy 1321 TCTCCGGGTAATGA 1335
Db 1321 TCTCCGGGTAATGA 1335

RESULT 2
AAC84208
ID AAC84208 standard; DNA; 1442 BP.
XX
AC AAC84208;
XX
DT 19-MAR-2001 (first entry)
XX
XX Plasmid Glambda-1Bpcd DNA sequence.
XX
DE Monoclonal antibody; F protein; respiratory syncytial virus; RSV;
KW Glambda-1; human; virucide; RSV propagation; ds.
XX
OS Homo sapiens.

xx PN WO200069462-A1.
xx PD 23-NOV-2000.
xx PF 18-MAY-2000; 2000WO-US13694.
xx PR 18-MAY-1999; 99US-0134702.
xx PA (SMIK) SMITHLINE BEECHAM CORP.
xx PI Gross MS, Sweet RW, Taylor G;
xx DR WPI; 2001-024947/03.
xx PT Human monoclonal antibody and functional fragments, useful for
PT therapeutic and/or prophylactic treatment of respiratory syncytial
PT virus infection, is specifically reactive with the F protein epitope of
PT the virus -
xx Claim 3, 6; Fig 10A-B; 102pp; English.
xx CC The invention provides a human monoclonal antibody (I) and its functional
CC fragments specifically reactive with an F protein epitope of respiratory
CC syncytial virus (RSV), and capable of neutralizing infection by the virus
CC such as Glambda-1A or Glambda-1B. The antibody can be expressed by
CC standard recombinant methodology. (I) is useful for detecting RSV by
CC contacting a source suspected of containing RSV with (I) and determining
CC whether (I) binds to the source. (I) is also useful for providing passive
CC immunotherapy prophylactically, to RSV disease in a human. (I) is useful
CC for therapeutic and/or prophylactic treatment of RSV infection in human
CC patients, particularly infants and young children. (I) is also useful
CC as a diagnostic reagent for the determination of RSV mediated disorders
CC or for tracking progress of treatment of the disorders. The present
CC sequence represents the continuous DNA sequence of the coding region of
CC the heavy chain of plasmid Glambda-1Bpcd.
xx SQ Sequence 1442 BP; 335 A; 458 C; 388 G; 261 T; 0 other;
Query Match 86.1%; Score 1149.2; DB 22; Length 1442;
Best Local Similarity 91.9%; Pred. No. 5.2e-215;
Matches 1246; Conservative 0; Mismatches 83; Indels 27; Gaps 2;
Qy 1 GAGTGTGACGTGGTGGAGTCTGGGGAGGCTTGTAAGCCCGGGGGTCCCTTAGACTC 60
Db 84 GAGTGTGACGTGGTGGAGTCTGGGGAGGCTTGTAAGCCCGGGGGTCCCTTAGACTC 143
Qy 61 TCCTGTGACGTAGCGGATTCACATTTTTCAGTGGCTTACGGATGCTTGGTCCGGCAGGCT 120
Db 144 TCCTGTGACGTAGCGGATTCACATTTTTCAGTGGCTTACGGATGCTTGGTCCGGCAGGCT 203
Qy 121 CCAGGGAAGGGGCTCGAGTGGTGGTGAATAGATTGAAATCTGATAATTATGCAACA 180
Db 204 CCAGGGAAGGGGCTCGAGTGGTGGTGAATAGATTGAAATCTGATAATTATGCAACA 257
Qy 191 CATATGCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
Db 258 CACTACTCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACACGCCATGAATCA 317
Qy 241 CTGTATCTGCAAAATGAACAGGCTGAAACCGGAGGACACAGCGGTGATTAATCTGT 294
Db 318 CTGTATCTGCAAAATGAACAGGCTGAAACCGGAGGACACAGCGGTGATTAATCTGT 377
Qy 295 -----ACAGATTTCATAGACTGGGGCCAGGGAACACTAGTACCGCTCTCC 339
Db 378 CAACCGGGGAGCTGGGGCCCTTTTGACCATTTGGGGCCAGGGAACCTTGGTACCGCTCTCC 437
Qy 340 TCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCTCTCTCCAAAGACACCTCT 399
Db 438 TCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCTCTCTCCAAAGACACCTCT 497
Qy 400 GGGGGCACAGGGCCCTGGGCTGGCTGCTAAGGACTACTTCCCGGAACCGGCTGACGGGT 459
|||||

Db 498 GGGGGCACAGGGCCCTGGGCTGCCCTGGTTCAGGAGTACTTCCCCGAACCCGGTGACGGTG 557
Qy 460 TCCTGGAACCTAGCGGCCCTTGACAGCGGCGTGCACACCTTCCCGGCTGTCTCTACAGTCC 519
Db 558 TCCTGGAACCTAGCGGCCCTTGACAGCGGCGTGCACACCTTCCCGGCTGTCTCTACAGTCC 617
Qy 520 TCAGGACTCTACTTCCCTCAGCAGCGGTGGTACCGTGGCCCTCCAGCAGCTTGGCAGCCAG 579
Db 618 TCAGGACTCTACTTCCCTCAGCAGCGGTGGTACCGTGGCCCTCCAGCAGCTTGGCAGCCAG 677
Qy 580 ACCTACATCTGCAACGTGAATCACAAGCCAGCAACCAACCAAGGTGGACAAGAAAGTGGAG 639
Db 678 ACCTACATCTGCAACGTGAATCACAAGCCAGCAACCAACCAAGGTGGACAAGAAAGTGGAG 737
Qy 640 CCCAAATCTTGACAAAACACTCACATGCCACCCAGTGGCCCGGAGCAGCTGAATCTGGGGGG 699
Db 738 CCCAAATCTTGACAAAACACTCACATGCCACCCAGTGGCCCGGAGCAGCTGAATCTGGGGGG 797
Qy 700 GCACCGCTCAGTCTTCTCTTCCCGCCAAAACCAAGGACACCCCTCATGATCTCCCGGACC 759
Db 798 GGACCGCTCAGTCTTCTCTTCCCGCCAAAACCAAGGACACCCCTCATGATCTCCCGGACC 857
Qy 760 CTTGAGTGCACATGCGTGGTGGTGGAGCTGAGCCAGCAAGACCCCTGAGGTCAAGTTCAAC 819
Db 858 CTTGAGTGCACATGCGTGGTGGTGGAGCTGAGCCAGCAAGACCCCTGAGGTCAAGTTCAAC 917
Qy 820 TGTAGCTGGACGGCTGGAGTGGATATATGCCAAGACAAGCCCGGGGAGGAGCAGTAC 879
Db 918 TGTAGCTGGACGGCTGGAGTGGATATATGCCAAGACAAGCCCGGGGAGGAGCAGTAC 977
Qy 880 AACAGCACGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 939
Db 978 AACAGCACGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1037
Qy 940 AAGAGTCAAGTGCAGAGTCTCCAAAGACCCCTCCAGCCCGCCATCGAGAAAACCATC 999
Db 1038 AAGAGTCAAGTGCAGAGTCTCCAAAGACCCCTCCAGCCCGCCATCGAGAAAACCATC 1097
Qy 1000 TCCAAAGCCAAAGGGCAGCCCGGAGAACACACAGGTGTACACCCCTGCCCGCATCCCGGGAT 1059
Db 1098 TCCAAAGCCAAAGGGCAGCCCGGAGAACACACAGGTGTACACCCCTGCCCGCATCCCGGGAT 1157
Qy 1060 GAGCTGACCAAGAACACAGGTTCAGCTTGCCTGGTCCAAAGGCTTCTTATCCAGCCGAC 1119
Db 1158 GAGCTGACCAAGAACACAGGTTCAGCTTGCCTGGTCCAAAGGCTTCTTATCCAGCCGAC 1217
Qy 1120 ATCCCGCTGGAGTGGAGAGCAATGGGAGCGGAGAGAACAACTACAAGACACAGCCTCC 1179
Db 1218 ATCCCGCTGGAGTGGAGAGCAATGGGAGCGGAGAGAACAACTACAAGACACAGCCTCC 1277
Qy 1180 GTGCTGAGCTCCGAGCGCTCTTCTTCTTCTTACAGCAAGCTCACCGTGGACAGAGCAGG 1239
Db 1278 GTGCTGAGCTCCGAGCGCTCTTCTTCTTCTTACAGCAAGCTCACCGTGGACAGAGCAGG 1337
Qy 1240 TGGCAGCAGGGGAACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1299
Db 1338 TGGCAGCAGGGGAACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1397
Qy 1300 ACAGCAAGAGCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1335
Db 1398 ACAGCAAGAGCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1433
RESULT 3
AAC98220
ID AAC98220 standard; cdNA; 1798 BP.
XX AAC98220;
XX AC
XX AAC98220;
XX 09-MAR-2001 (first entry)
XX Human colon cancer antigen nucleotide sequence SEQ ID NO:230.
XX

KW	Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW	identification; cytostatic; cardioactive; neuroprotective; vulnery;
KW	immunomodulatory; muscular; gynaecological; gastrointestinal;
KW	nephrotropic; antineoplastic; antibacterial; gene therapy; wound;
KW	neural disorder; immune system disorder; muscular disorder;
KW	reproductive disorder; gastrointestinal disorder; renal disorder;
KW	infectious disease; cardiovascular disorder; ss.
OS	Homo sapiens.
XX	WO2000055351-A1.
PN	21-SEP-2000.
PD	
XX	
PF	08-MAR-2000; 2000WO-US05883.
XX	
PR	12-MAR-1999; 99US-0124270.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Rosen CA, Ruben SM;
XX	
DR	WPI; 2000-587534/55.
DR	P-PSDB; AAB53463.
XX	
PT	Colon cancer associated gene sequences, referred to as colon cancer
PT	antigens, useful for the treatment, prevention, and diagnosis of colon
PT	disorders such as colon cancer.
XX	
PS	Claim 1; Page 652; 2104pp; English.
XX	
CC	CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC	called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC	human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC	neuroprotective, immunomodulatory, gynaecological, gastrointestinal, and
CC	vulnery, nephrotropic, antineoplastic and antibacterial activities, and
CC	can be used in gene therapy. The colon cancer antigen polynucleotides,
CC	proteins and antibodies to the proteins are useful for the prevention,
CC	treatment and diagnosis of colon disorders, such as colon cancer. The
CC	polynucleotides may be used in diagnostics and research, such as for
CC	chromosome identification, and as hybridisation probes. The proteins
CC	may also be used to prevent diseases such as neural disorders, immune
CC	system disorders, muscular disorders, reproductive disorders,
CC	gastrointestinal disorders, wounds, renal disorders, infectious
CC	diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
CC	AAB54007 represent sequences used in the exemplification of the present
CC	invention.
XX	
QY	Sequence 1798 BP; 477 A; 529 C; 458 G; 311 T; 23 other;
XX	
QY	Query Match 86.0%; Score 1147.8; DB 21; Length 1798;
XX	Best Local Similarity 91.0%; Pred. No. 9.9e-215;
XX	Matches 1245; Conservative 10; Mismatches 73; Indels 40; Gaps
QY	2 AGGTGCAGCTGGTGGAGCTGGGGAGGCTGTGAAGCCGGGGGTCCTTAGACTCT 61
DB	206 AGTGCAGCTGGTGGAGCTGGGGAGGCGCTGCAGCTCGGAGGCTCCTGAGACTCT 265
QY	62 CCTGTGCAGCTAGCGGATTCACCTTTTCAGTGGCTACTGGATGTCCTGGGTCCGGCAGGCTC 121
DB	266 CCTGTGCAGCTCCTGGATTCACCTTCAGTAGCTATGTCATGTCAGTGGTCCGGCAGGCTC 325
QY	122 CAGGGAAGGGCTCGAGTGGTGGTTCGGAATAGATTGAATCTGATATTTATTCGAACAC 181
DB	326 CAGGCAAGGGCTCGAGTGGTGGTGGCAGTTATATTS-----RTATGATGAAGTAATTAAT 379
QY	182 ATTATCGCGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241
DB	380 ACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCAGAACACGC 439
QY	242 TGTATCTGCAAAATGAACAGCCTGAAACCGAGGACACAGCCGTGTATTTACTGTACAGATT 301
DB	440 TGTATCTGCAAAATGAACAGCCTGAGAGCTGAGGACCGGTGTTATTTACTGTGCGAAG 499

QY	796	GAAGACCCCTGAGGTCAAGTTCAACTTGGGTACGTGGACGGCTGGAGGTGCATATAATGCCAAG	855
Db	898	GAAGACCCCTGAGGTCAAGTTCAACTTGGGTACGTGGACGGCTGGAGGTGCATATAATGCCAAG	957
QY	856	ACAAAGCCCGGGAGGAGCAGTACAAACGACGATACCGTGTGGTACGCGTCTCACCGTC	915
Db	958	ACAAAGCCCGGGAGGAGCAGTACAAACGACGATACCGTGTGGTACGCGTCTCACCGTC	1017
QY	916	CTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTCCAAGGTCTCCAACAAAGCCCTC	975
Db	1018	CTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTCCAAGGTCTCCAACAAAGCCCTC	1077
QY	976	CCAGCCCCCATCGAGAAACCACTCTCCAAGCCAAAGGCGACGCCCGGAGAACCAAGGTG	1035
Db	1078	CCAGCCCCCATCGAGAAACCACTCTCCAAGCCAAAGGCGACGCCCGGAGAACCAAGGTG	1137
QY	1036	TACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGGTCAAGCTGACCTGCCTG	1095
Db	1138	TACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGGTCAAGCTGACCTGCCTG	1197
QY	1096	GTCAAAGGCTTCTATCCCAAGCAGCATCGCGGTGGAGTGGGAGAGCAATGGGCGACCGGAG	1155
Db	1198	GTCAAAGGCTTCTATCCCAAGCAGCATCGCGGTGGAGTGGGAGAGCAATGGGCGACCGGAG	1257
QY	1156	AACAACCTACAAGACCAAGCGCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGC	1215
Db	1258	AACAACCTACAAGACCAAGCGCTCCCGTGTGGACTCCGACGGCTCCTTCTTCTCTACAGC	1317
QY	1216	AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGCGGACGTCTTCTATGCTCCGTGATG	1275
Db	1318	AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGCGGACGTCTTCTATGCTCCGTGATG	1377
QY	1276	CATGAGGCTCTGCACAAACCACTACAGCAGAAGAGCCCTCCCTGTCTCCGGGTAAATGA	1335
Db	1378	CATGAGGCTCTGCACAAACCACTACAGCAGAAGAGCCCTCCCTGTCTCCGGGTAAATGA	1437
RESULT 6			
AA113847			
ID	AA113847 standard; DNA; 1437 BP.		
XX			
AC	AA113847;		
XX			
DT	25-MAY-1997 (first entry)		
XX			
DE	Primitised anti-human B7.1 antigen antibody 7B6 heavy chain DNA.		
XX			
KW	Monoclonal antibody; cynomolgus monkey; macaque; 7B6;		
KW	primitised antibody; B7 antigen; CD28; immunosuppressive;		
KW	autoimmune disease; idiopathic thrombocytopaenia purpura;		
KW	systemic lupus erythematosus; rheumatoid arthritis; psoriasis;		
KW	type 1 diabetes mellitus; graft versus host disease;		
KW	hetero-hybridoma; transfectoma; ss.		
XX			
OS	Chimeric Macaca cynomolgus;		
OS	Chimeric Homo sapiens.		
XX			
PN	WO9640878-A1.		
XX			
PD	19-DEC-1996.		
XX			
PF	06-JUN-1996; 96WO-US10053.		
XX			
PR	07-JUN-1995; 95US-0487550.		
XX			
XX	(IDEC-) IDEC PHARM CORP.		
XX			
PI	Anderson DR, Brans P, Hanna N, Shestowsky WS;		
XX			
DR	WPI; 1997-108638/10.		
DR	P-PSDB; AAW01820.		
XX			

PT	Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PF	useful for treating autoimmune disease or graft-versus-host disease
XX	
PS	Claim 8; Fig 9B; 81pp; English.
XX	
CC	2 DNA sequences (AAT62511 and AAT13847) respectively code for
CC	primatised forms (AAW01819 and AAW01820) of the light and heavy chains
CC	of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody
CC	7B6.. Cloned 7B6 light and heavy variable genes are inserted into
CC	an expression vector (pref. NEOSPLA) which contains human light and
CC	heavy chain constant region genes to allow prodn. of primatised
CC	antibody in e.g. CHO cells. Primatised 7C10 and 16C10 anti-B7.1
CC	antibodies have also been produced (see also AAW01817-18 and AAW01821-
CC	22). The primatised antibodies inhibit the B7:CD28 pathway, making
CC	them useful immunosuppressants for the treatment of autoimmune
CC	disorders and graft-versus-host disease.
XX	
SQ	Sequence 1437 BP; 329 A; 452 C; 387 G; 269 T; 0 other;
	Query Match 85.8%; Score 1145.6; DB 18; Length 1437;
	Best Local Similarity 90.7%; Pred. No. 2.6e-214;
	Matches 1251; Conservative 0; Mismatches 84; Indels 45; Gaps 1;
QY	1 GAGGTGCAGCTGTTGGAGTCTGGGGAGCGCTTGTAAGACGCCGGGGGTCCCTTAGACTC 60
DB	
QY	58 GAGGTGCAACTGGTGGAGTCTGGGGAGCGCTTGTTCCAGCTGGCGGGTCCCTGAGAGTC 117
QY	61 TCCTCTGCAGCTAGCGGAATTCACTTTCAGTGGCTACTGCATCTCTCGTGGTCCGCCAGCT 120
DB	
QY	118 TCCTCTGCAGTCTCTGGATTCACCTTCTAGTGACCACACTCATGTATGTTGTTCCGCCAGCT 177
QY	121 CCAGGAAGGGGCTCGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATATGCAACA 180
DB	
QY	178 CCAGGAAGGGGCGGAATGGTAGTTTCTATTAGAACAACCAACGCGTGGGACACA 237
QY	181 CATATGCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATCAAATCTAGA 240
DB	
QY	238 GAATACGGCGGCTGTGTGAAAGACAGATTCACCATCTCCAGAGATGATTCAAAAGCATC 297
QY	241 CTGTATCTGCAAAATCAACAGCTGTAACACCGAGGACACAGCGCTGATTACTGTGAC --- 296
DB	
QY	298 GCCTATCTGCAAAATGACAGCGCTGAAATCTCAGGACACAGCGCGCTATTACTGTACTACA 357
QY	297 -----AGATTTTCATAGACTGGGCG 315
DB	
QY	316 CAGGGAACACATAGTCACCGTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCGCTG 375
DB	
QY	418 CAGGCGCGCTGGTCCACCGTCTCTCTCAGCTAGCACCAAGGGCCCCATCGTCTTCCCGCTG 477
QY	376 GCACCTCTCCAAGAGCACCTCTCGGGGACAGCGGCCCTCGGTGCTGCTCAAGAC 435
DB	
QY	436 TACTTCCCAGAACCGGTGACGGTGTCTGGAACTCAGCGGCCCTGACCGGGCGGTGCAC 495
DB	
QY	538 TACTTCCCAGAACCGGTGACGGTGTCTGGAACTCAGCGGCCCTGACCGGGCGGTGCAC 597
QY	496 ACCTTCCCGGCTGCTCTACAGTCTCAGAGCTCTACTCCCTCAGCAGCGTGGTGCACGTG 555
DB	
QY	598 ACCTTCCCGGCTGCTCTACAGTCTCAGAGCTCTACTCCCTCAGCAGCGTGGTGCACGTG 657
QY	556 CCTCCAGCAGCTTGGGACCCAGACCTTACATCTGCAGGTGAATCAACGCCAGCAAC 615
DB	
QY	658 CCTCCAGCAGCTTGGGACCCAGACCTTACATCTGCAACGTGAATCAACGCCAGCAAC 717
QY	616 ACCAAGGTGGACAAGAAAGTGAGGCCCAAACTCTGTGACAAACTCACACATGCCCCACG 675
DB	
QY	718 ACCAAGGTGGACAAGAAAGTGAGGCCCAAACTCTGTGACAAACTCACACATGCCCCACG 777
QY	676 TGCCCGACGACCTGAACCTCGCGGGGACCGCTCAGTCTTCTCTTCCCGCCCAAAACCCCAAG 735


```
QY 430 AAGGACTACTTCCCGAACCAGGTGACGGTGTGCGTGAAGTCTCAGGCGCCTGACAGCGG 489
DB 481 AAGGACTACTTCCCGAACCAGGTGACGGTGTGCGTGAAGTCTCAGGCGCCTGACAGCGG 540
QY 490 GTGCACACTTCCCGGCTGTCTCAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGT 549
DB 541 GTGCACACTTCCCGGCTGTCTCAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGT 600
QY 550 ACCGTGCTCCAGCAGCTTGGGACCCAGACCTACATCTCAAGTGAATCAAGGCC 609
DB 601 ACCGTGCTCCAGCAGCTTGGGACCCAGACCTACATCTCAAGTGAATCAAGGCC 660
QY 610 AGCAACCAAGGTGGACAAGAAAGTGGAGCCCAAAATCTGTGCAAACTCAACATGC 669
DB 661 AGCAACCAAGGTGGACAAGAAAGTGGAGCCCAAAATCTGTGCAAACTCAACATGC 720
QY 670 CCACGTGCCAGCAGCTGAAGTCCGGGGGACCGGTACGTCAGTCTTCCCTCCCAAAA 729
DB 721 CCACGTGCCAGCAGCTGAAGTCCGGGGGACCGGTACGTCAGTCTTCCCTCCCAAAA 780
QY 730 CCCAAGGACACCTCATGATCTCCGGGACCCCTGAGGTACATCGTGGTGGTGGAGTG 789
DB 781 CCCAAGGACACCTCATGATCTCCGGGACCCCTGAGGTACATCGTGGTGGTGGAGTG 840
QY 790 AGCCACGAAGACCCCTGAGGTCAAGTTCAGTTCAGTGGAGCGCGTGGAGTGCATAAT 849
DB 841 AGCCACGAAGACCCCTGAGGTCAAGTTCAGTTCAGTGGAGCGCGTGGAGTGCATAAT 900
QY 850 GCCAAGACAAAGCCCGGAGGAGCAGTACAAACAGCAGTACCGTGGTGGTGGTGGTGC 909
DB 901 GCCAAGACAAAGCCCGGAGGAGCAGTACAAACAGCAGTACCGTGGTGGTGGTGGTGC 960
QY 910 ACCGTCTGTCACAGGACTGGCTGAATGCGAAGGAGTACAAGTCAAGTCTCCCAACAA 969
DB 961 ACCGTCTGTCACAGGACTGGCTGAATGCGAAGGAGTACAAGTCAAGTCTCCCAACAA 1020
QY 970 GCCCTCCAGCGCCCATCGAAGAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCA 1029
DB 1021 GCCCTCCAGCGCCCATCGAAGAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCA 1080
QY 1030 CAGGTGTACACCTCCGCGGATGAGTACCAAGACCAAGACCAAGTCCAGCTGACC 1089
DB 1081 CAGGTGTACACCTCCGCGGATGAGTACCAAGACCAAGACCAAGTCCAGCTGACC 1140
QY 1090 TGCCTGGTCAAGAGTCTTATCCAGCGACATCGCGGTGGAGTGGAGCAATGGGCG 1149
DB 1141 TGCCTGGTCAAGAGTCTTATCCAGCGACATCGCGGTGGAGTGGAGCAATGGGCG 1200
QY 1150 CCGGAGACAACTACAAGACACGCTCCCGTGTGGACTCCGAGCGCTCTCTTCTGCTC 1209
DB 1201 CCGGAGACAACTACAAGACACGCTCCCGTGTGGACTCCGAGCGCTCTCTTCTGCTC 1260
QY 1210 TACAGCAAGCTCACCGTGGACAAGAGCAGTGGCAGAGGGAAGTCTTCTCATGCTCC 1269
DB 1261 TACAGCAAGCTCACCGTGGACAAGAGCAGTGGCAGAGGGAAGTCTTCTCATGCTCC 1320
QY 1270 GTGATGATAGGCTCTGCACAACCACTACAGCGAGAGAGCGCTCTCCCTGTCTCCGGGT 1329
DB 1321 GTGATGATAGGCTCTGCACAACCACTACAGCGAGAGAGCGCTCTCCCTGTCTCCGGGT 1380
QY 1330 AATGA 1335
DB 1381 AATGA 1386
```

RESULT 10

```
AAC84206
ID AAC84206 standard; DNA; 6281 BP.
XX
AC AAC84206;
XX
DT 19-MAR-2001 (first entry)
XX
```

```
DE Plasmid Glambda-lApcd DNA sequence.
XX
KW Monoclonal antibody; F protein; Respiratory syncytial virus; RSV;
KW Glambda-1; human; virucide; RSV propagation; ds.
XX
OS Homo sapiens.
XX
PN WO200069462-A1.
XX
PD 23-NOV-2000.
XX
PF 18-MAY-2000; 2000WO-US13694.
XX
PR 18-MAY-1999; 99US-0134702.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI Gross MS, Sweet RW, Taylor G;
XX
WI; 2001-024947/03.
XX
PT Human monoclonal antibody and functional fragments, useful for
PT therapeutic and/or prophylactic treatment of respiratory syncytial
PT virus infection, is specifically reactive with the F protein epitope of
PT the virus -
XX
PS Claim 6; Fig 8A-F; 102pp; English.
XX
CC The invention provides a human monoclonal antibody (I) and its functional
CC fragments specifically reactive with an F protein epitope of respiratory
CC syncytial virus (RSV), and capable of neutralizing infection by the virus
CC such as Glambda-1A or Glambda-1B. The antibody can be expressed by
CC standard recombinant methodology. (I) is useful for detecting RSV by
CC contacting a source suspected of containing RSV with (I) and determining
CC whether (I) binds to the source. (I) is also useful for providing passive
CC immunotherapy prophylactically, to RSV disease in a human. (I) is useful
CC for therapeutic and/or prophylactic treatment of RSV infection in human
CC patients, particularly infants and young children. (I) is also useful
CC as a diagnostic reagent for the determination of RSV mediated disorders
CC or for tracking progress of treatment of the disorders. The present
CC sequence represents the continuous DNA sequence of the expression plasmid
CC Glambda-lApcd containing the RSV neutralising human Glambda-1 mAb for the
CC heavy chain.
XX
SQ Sequence 6281 BP; 1555 A; 1634 C; 1618 G; 1474 T; 0 other;

Query Match 85.6%; Score 1142.8; DB 22; Length 6281;
Best Local Similarity 91.8%; Pred. No. 1e-213;
Matches 1242; Conservative 0; Mismatches 87; Indels 27; Gaps 2;

QY 1 GAGTGTGAGTGTGGAGTCTGGGGAGGCTTGGTAAAGCCGGGGGTCCCTTAGACTC 60
DB 1072 GAGTGTGAGTGTGGAGTCTGGGGAGGCTTGGTAAAGCCGGGGGTCCCTTAGACTC 1131
QY 61 TCCTGTGAGTGTGGAGTCTGGGGAGGCTTGGTAAAGCCGGGGGTCCCTTAGACTC 120
DB 1132 TCCTGTGAGTGTGGAGTCTGGGGAGGCTTGGTAAAGCCGGGGGTCCCTTAGACTC 1191
QY 121 CCAGGGAAGGGGTCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 180
DB 1192 CCAGGGAAGGGGTCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1245
QY 181 CATTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
DB 1246 CATTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 1305
QY 241 CTGTATCTGCAATGACAGCCTGAAAACCGAGGACACAGCCGTGTTACTGT----- 294
DB 1306 CTGTATCTGCAATGACAGCCTGAAAACCGAGGACACAGCCGTGTTACTGT----- 1365
QY 295 -----ACAGATTTCTAGACTGGGGCCAGGGAACACTAGTACCGTCTCC 339
DB 1366 CAACCGGGGAGTGGCGCCTTTTGACCATTTGGGGCCAGGGAACCGTGGTACCGTCTCC 1425
```

```
QY 340 TCAGCCTCCACCAAGGCCCATCGGTCTTCCCTCCGACCCCTCCCTCCCAAGAGCACTCT 399
D 1426 TCAGCCTCCACCAAGGCCCATCGGTCTTCCCTCCGACCCCTCCCTCCCAAGAGCACTCT 1485
QY 400 GGGGGACACAGCGCCCTGGCGCTGCTGGTCAAGAGTACTTCCCGCAACCGGTGACGGTG 459
D 1486 GGGGGACACAGCGCCCTGGCGCTGCTGGTCAAGAGTACTTCCCGCAACCGGTGACGGTG 1545
QY 460 TCGTGAACCTCAGCGCCCTGACAGCGCGTGCACACCTTCCCGCTGTCTACAGTCC 519
D 1546 TCGTGAACCTCAGCGCCCTGACAGCGCGTGCACACCTTCCCGCTGTCTACAGTCC 1605
QY 520 TCAGGACTCTACTCCCTTCAGCAGCGGTGGTGAACCGTCCCTCCAGCAGCTTGGSCACCCAG 579
D 1606 TCAGGACTCTACTCCCTTCAGCAGCGGTGGTGAACCGTCCCTCCAGCAGCTTGGSCACCCAG 1665
QY 580 ACCTACATCTGCAACGTGATCACAAGCCCAAGCAACCAAGGTGACAAAGTGGAG 639
D 1666 ACCTACATCTGCAACGTGATCACAAGCCCAAGCAACCAAGGTGACAAAGTGGAG 1725
QY 640 CCCAAATCTTGTGACAAAACCTACACATGCCACCGTGGCCAGCCTGAACCTCGCGGG 699
D 1726 CCCAAATCTTGTGACAAAACCTACACATGCCACCGTGGCCAGCCTGAACCTCGCGGG 1785
QY 700 GCACCGTCACTCTCTCTTCCCTCCCAAAACCAAGCAACCGTCTATGATCTCCCGGACC 759
D 1786 GGACCGTCACTCTCTCTTCCCTCCCAAAACCAAGCAACCGTCTATGATCTCCCGGACC 1845
QY 760 CTTGAGTCACTCGTGGTGGTGGACGTGAGCCAGCAAGACCGCTCAGTCAAGTCAAC 819
D 1846 CTTGAGTCACTCGTGGTGGTGGACGTGAGCCAGCAAGACCGCTCAGTCAAGTCAAC 1905
QY 820 TGTGACGTGACGCGGTGGAGGTGCATAATGCCAAGCAAAAGCGGGAGGAGCAGTAC 879
D 1906 TGTGACGTGACGCGGTGGAGGTGCATAATGCCAAGCAAAAGCGGGAGGAGCAGTAC 1965
QY 880 AACAGACGTACCGTGTGTCAGCTCTCTACCGTCTCGCAGGACGTGGCTGAATGCG 939
D 1966 AACAGACGTACCGTGTGTCAGCTCTCTACCGTCTCGCAGGACGTGGCTGAATGCG 2025
QY 940 AAGGAGTACAAGTGCAAGGTCTCCAAAGACCGCTCCAGCCCGCCATCGAGAAAACCATC 999
D 2026 AAGGAGTACAAGTGCAAGGTCTCCAAAGACCGCTCCAGCCCGCCATCGAGAAAACCATC 2085
QY 1000 TCCAAAGCCAAAGGAGCGAGCCCGGAGAACACAGGTGTACACCGTCCCGCCATCCCGGGAT 1059
D 2086 TCCAAAGCCAAAGGAGCGAGCCCGGAGAACACAGGTGTACACCGTCCCGCCATCCCGGGAT 2145
QY 1060 GAGCTGACCAAGAACCGAGGTCAACCTGACCTGCCTGGTCAAGGGCTTATCCCGAGCGAC 1119
D 2146 GAGCTGACCAAGAACCGAGGTCAACCTGACCTGCCTGGTCAAGGGCTTATCCCGAGCGAC 2205
QY 1120 ATCCCGCTGGAGTGGGAGAGCAATGGCGAGCGGAGAACAACTACAAAGACCAAGCGCTCC 1179
D 2206 ATCCCGCTGGAGTGGGAGAGCAATGGCGAGCGGAGAACAACTACAAAGACCAAGCGCTCC 2265
QY 1180 GTGCTGACTCCGAGCGGTCTCTTCTCTCTACAGCAAGCTCACCCTGACAAAGAGCAGG 1239
D 2266 GTGCTGACTCCGAGCGGTCTCTTCTCTCTACAGCAAGCTCACCCTGACAAAGAGCAGG 2325
QY 1240 TGGCAGCAGGGGAACCTCTCTCATGCTCCGTGATCATGAGGCTCTGCACAAACACTAC 1299
D 2326 TGGCAGCAGGGGAACCTCTCTCATGCTCCGTGATCATGAGGCTCTGCACAAACACTAC 2385
QY 1300 ACSCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1335
D 2386 ACSCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 2421
```

RESULT 11
AAV61794
ID

AAV61794 standard; DNA; 19035 BP.

```
XX AAV61794;  
AC  
XX  
DT 07-JUN-1999 (first entry)  
XX  
DE Traget plasmid Mandy containing anti-CD23 gene.  
XX  
KW Mandy; target plasmid; gene integration; gene amplification;  
KW homologous recombination; vector; neomycin phosphotransferase;  
KW neo gene; selectable marker; immunoglobulin; CD23; 5B8; human; ss.  
XX  
OS Chimeric - Mus sp.  
OS Chimeric - Escherichia coli.  
OS Chimeric - Baculovirus.  
OS Chimeric - Cytomegalovirus.  
OS Chimeric - Rhesus macaque polyoma virus.  
OS Chimeric - Photinus sp.  
OS Chimeric - Salmonella typhimurium.  
OS Chimeric - Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT misc_feature 361  
FT /*tag= a  
FT /note= "this base represents a nucleotide missing  
FT from the sequence given in the  
FT specification. It is included to  
FT maintain the nucleotide numbering in the  
FT specification for this sequence"  
FT  
FT misc_feature 721  
FT /*tag= b  
FT /note= "this base represents a nucleotide missing  
FT from the sequence given in the  
FT specification. It is included to  
FT maintain the nucleotide numbering in the  
FT specification for this sequence"  
FT  
FT misc_feature 2941  
FT /*tag= c  
FT /note= "this base represents a nucleotide missing  
FT from the sequence given in the  
FT specification. It is included to  
FT maintain the nucleotide numbering in the  
FT specification for this sequence"  
FT  
FT misc_feature 3301  
FT /*tag= d  
FT /note= "this base represents a nucleotide missing  
FT from the sequence given in the  
FT specification. It is included to  
FT maintain the nucleotide numbering in the  
FT specification for this sequence"  
FT  
FT misc_feature 4261  
FT /*tag= e  
FT /note= "this base represents a nucleotide missing  
FT from the sequence given in the  
FT specification. It is included to  
FT maintain the nucleotide numbering in the  
FT specification for this sequence"  
FT  
FT misc_feature 4621..4622  
FT /*tag= f  
FT /note= "these bases represent nucleotides missing  
FT from the sequence given in the  
FT specification. They are included to  
FT maintain the nucleotide numbering in the  
FT specification for this sequence"  
FT  
FT misc_feature 8161  
FT /*tag= g  
FT /note= "this base represents a nucleotide missing  
FT from the sequence given in the  
FT specification. It is included to  
FT maintain the nucleotide numbering in the  
FT specification for this sequence"  
FT  
FT misc_feature 8521..8522  
FT /*tag= h  
FT /note= "these bases represent nucleotides missing  
FT from the sequence given in the  
FT specification. It is included to  
FT maintain the nucleotide numbering in the  
FT specification for this sequence"
```


FT from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"

FT 12061
FT /tag=
FT /note="this base represents a nucleotide missing
FT from the sequence given in the
FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"

FT 12421
FT /tag=
FT /note="these bases represent nucleotides missing
FT from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"

FT 13381
FT /tag=
FT /note="this base represents a nucleotide missing
FT from the sequence given in the
FT specification. It is included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"

FT 14641
FT /tag=
FT /note="these bases represent nucleotides missing
FT from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"

FT 15001
FT /tag=
FT /note="these bases represent nucleotides missing
FT from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"

FT 15961
FT /tag=
FT /note="these bases represent nucleotides missing
FT from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"

FT 16321
FT /tag=
FT /note="these bases represent nucleotides missing
FT from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"

FT 16321
FT /tag=
FT /note="these bases represent nucleotides missing
FT from the sequence given in the
FT specification. They are included to
FT maintain the nucleotide numbering in the
FT specification for this sequence"

XX WO9841645-A1.
PN 24-SEP-1998.
PD 09-MAR-1998; 98WO-US03935.
PF 13-FEB-1998; 98US-0023715.
PR 14-MAR-1997; 97US-0819866.
XX (IDEC-) IDEC PHARM CORP.
XX Barnett RS, McLachlan KR, Reff ME;
PI WPI; 1998-521229/44.
XX Site specific integration of DNA in mammals for expressing, e.g.
PT immunoglobulins - comprises homologous recombination using
PT selectable marker and target plasmids.
XX

PS Example 1; Fig 10; 114pp; English.
XX This is the nucleotide sequence of novel target plasmid Mandy.
CC The plasmid includes an inactivated murine dihydrofolate reductase
CC (DHFR) gene, the Escherichia coli beta-galactosidase gene,
CC baculovirus DNA, a cassette comprising the promoter and enhancer
CC elements from cytomegalovirus and SV40 virus, the E. coli
CC beta-glucuronidase (GUS) gene, firefly luciferase gene, an
CC inactivated Salmonella typhimurium histidinol dehydrogenase (HisD)
CC gene and transposon Tn5 neomycin phosphotransferase (neo) gene
CC sequences, in a pBR-derived backbone, and also an anti-human CD23
CC IgE receptor human gamma-1 monoclonal antibody 5E8 gene. The
CC invention provides a novel method for integrating a desired
CC exogenous DNA at a target site within the genome of a mammalian
CC cell via homologous recombination. This involves transfecting the
CC cell with a 'marker plasmid' such as Desmond (see AAV61793), which
CC contains a unique sequence that is foreign to the mammalian cell
CC genome and which provides a substrate for homologous recombination,
CC followed by transfection with a 'target plasmid', such as Mandy
CC or Molly (see AAV61793), containing a sequence which provides for
CC homologous recombination with the unique sequences contained in
CC the marker plasmid, and further comprising a desired DNA that is
CC to be integrated into the mammalian cells, typically an
CC immunoglobulin or other secreted mammalian glycoprotein. The
CC homologous recombination system utilises the neo gene as a
CC dominant selectable marker. The neo gene is split into 3 exons.
CC Exon 3 is present on the marker plasmid and becomes integrated
CC into the host cell genome upon integration of the marker plasmid
CC into the mammalian cells. Exons 1 and 2 are present on the
CC targeting plasmid, and are separated by an intron into which at
CC least one gene of interest is cloned. Homologous recombination
CC of the targeting vector with the integrated marking vector results
CC in correct splicing of all 3 exons of the neo gene and expression
CC of a functional neo protein. The method is applicable to all
CC mammalian cells, and can be used to express any type of recombinant
CC protein. The use of a triply spliced selectable marker means that
CC all selected colonies arise from homologous recombination. In
CC addition, the number of colonies that need to be screened to
CC identify high producer clones is reduced. An amplifiable gene can
CC be inserted on integration of the marking vector, so that when a
CC gene is targeted to this site, the gene is further enhanced by gene
CC amplification.

XX Sequence 19035 BP; 4705 A; 4968 C; 4822 G; 4519 T; 21 other;
SQ

Query Match 85.6%; Score 1142.2; DB 19; Length 19035;
Best Local Similarity 92.1%; Pred. No. 1.5e-213;
Matches 1246; Conservative 0; Mismatches 83; Indels 24; Gaps 3;

QY 1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
DB 9489 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 9548
QY 61 TCCTGTGCAGCTAGCG-----GATTCACCTTTCAGTGGCTAGTGGATGCTCTGGTCCGC 114
DB 9549 TCCTGTGCAGCTAGCGCTCCGGGTTTCAGGTTTCAATTAACCTACTACATGAGTGGTCCGC 9608
QY 115 CAGGCTCCAGGAGGGGCTCGAGTGGTTCCTCAATTAGATTGAATCGATTAATAT 174
DB 9609 CAGGCTCCAGGAGGGGCTCGAGTGGTTCCTCAATTAGATTGAATCGATTAATAT 174
QY 175 GCAACACATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAA 234
DB 9663 CCCACATGGTACGAGACTCCGTGAAGGCGAGATTCACCATCTCCAGAGAGAGCCCAAG 9722
QY 235 TCTAGACTGTATCTGCAAAATGAACAGCCTGAAACACGAGGACACAGCCGGTGTATTACTG- 293
DB 9723 AACACACTGTTTCTTCAAAATGAACAGCCTGAGAGCTGAGGACGAGCTGTCTATTACTGT 9782
QY 294 -----TACAGATTTTCATAGACTGGGGCCAGGAGACACTAGTACCGTCTCTCA 342
DB 9783 GCGAGCTTGACTACAGGGTCTGACTCTCTGGGGCCAGGAGTCTCTGGTTCACCGTCTCTCA 9842

```
QY 343 CCCTCCACCAAGGGCCATCGGTCTTCCCGCTGGCACCCTCTCTCCCAAGACACCTCTGGG 402
Db 9843 GCTAGACCAAGGGCCATCGGTCTTCCCGCTGGCACCCTCTCTCCCAAGACACCTCTGGG 9902
QY 403 GGCACAGGGCCCTGGGCTGCTGCTCAAGACTACTTCCCGAAGCGGTGACGGTCTCG 462
Db 9903 GGCACAGGGCCCTGGGCTGCTGCTCAAGACTACTTCCCGAAGCGGTGACGGTCTCG 9962
QY 463 TGGAACTCAGGCGCCCTGACAGCGGGTGCACACCTTCCCGGTGTCTTACAGTCTCTCA 522
Db 9963 TGGAACTCAGGCGCCCTGACAGCGGGTGCACACCTTCCCGGTGTCTTACAGTCTCTCA 10022
QY 523 GGACTCTACTCTCCCTACAGAGGGTGTGACCGTGCCTCTCCAGAGCTTGGGACCCAGAC 582
Db 10023 GGACTCTACTCTCCCTACAGAGGGTGTGACCGTGCCTCTCCAGAGCTTGGGACCCAGAC 10082
QY 583 TACATCTGCAAGCTGAATCACAAGCCCAAGCAACACCAAGGTGACAGAAGGTGAGCC 642
Db 10083 TACATCTGCAAGCTGAATCACAAGCCCAAGCAACACCAAGGTGACAGAAGGTGAGCC 10142
QY 643 AAATCTTGTGACAAACTACATGCCCCACCGTGGCCAGCACCTGAATCTGGCGGGGCA 702
Db 10143 AAATCTTGTGACAAACTACATGCCCCACCGTGGCCAGCACCTGAATCTGGCGGGGCA 10202
QY 703 CCGTCAGTCTCTCTTCCCGCCCAAAACCAAGAGACACCTCATGATCTCCCGGACCCCT 762
Db 10203 CCGTCAGTCTCTCTTCCCGCCCAAAACCAAGAGACACCTCATGATCTCCCGGACCCCT 10262
QY 763 GAGTCACATCGGTGTGGTGGAGCTGAGCCAGAGACACCTGAGGTCAAGTTCAACTGG 822
Db 10263 GAGTCACATCGGTGTGGTGGAGCTGAGCCAGAGACACCTGAGGTCAAGTTCAACTGG 10322
QY 823 TACGTGACGGCTGGAGGTGCATATGCCAAGAAAGCCGCGGAGAGAGCAATCAAC 882
Db 10323 TACGTGACGGCTGGAGGTGCATATGCCAAGAAAGCCGCGGAGAGAGCAATCAAC 10382
QY 883 AGCAGCTACCGTGTGGTGCCTCCTCAGCTGCTCAGCAGGACCTGGCTGAATGCAAG 942
Db 10383 AGCAGCTACCGTGTGGTGCCTCCTCAGCTGCTCAGCAGGACCTGGCTGAATGCAAG 10442
QY 943 GAGTACAGTGCAGGTCTCCAAAGCCCTCCAGCCCGCCATCGAGAAACCATCTCC 1002
Db 10443 GAGTACAGTGCAGGTCTCCAAAGCCCTCCAGCCCGCCATCGAGAAACCATCTCC 10502
QY 1003 AAAGCCAAAGGGAGCGCCCGAGAACACAGGTGTACACCTGCCCGCATCCCGGGATGAG 1062
Db 10503 AAAGCCAAAGGGAGCGCCCGAGAACACAGGTGTACACCTGCCCGCATCCCGGGATGAG 10562
QY 1063 CTGACCAAGAACACAGGTGTACCTGCTGCTCCTCAAGGCTTCTATCCAGCGACATC 1122
Db 10563 CTGACCAAGAACACAGGTGTACCTGCTGCTCCTCAAGGCTTCTATCCAGCGACATC 10622
QY 1123 GCCGTGGAGTGGGAGAGCAATGGCGAGCGGAGAGCAACTACAAGACACCGCTCCCGTG 1182
Db 10623 GCCGTGGAGTGGGAGAGCAATGGCGAGCGGAGAGCAACTACAAGACACCGCTCCCGTG 10682
QY 1183 CTGGACTCCAGCGCTCTCTCTCTCTACAGCAAGCTCACCGTGACAAAGAGCAGGTGG 1242
Db 10683 CTGGACTCCAGCGCTCTCTCTCTCTACAGCAAGCTCACCGTGACAAAGAGCAGGTGG 10742
QY 1243 CAGCAGGGGAACCTCTCTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACAG 1302
Db 10743 CAGCAGGGGAACCTCTCTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACAG 10802
QY 1303 CAGAAGAGCCTCTCCCTGTGTCTCCGGGTAATGA 1335
Db 10803 CAGAAGAGCCTCTCCCTGTGTCTCCGGGTAATGA 10835
RESULT 12
AAV41431
ID AAV41431 standard; DNA; 1427 BP.
XX
```

```
AC AAV41431;
XX
DT 12-OCT-1998 (first entry)
DE Plasmid Hu19CHcpd encoding anti-RSV F protein Hu19C heavy chain.
XX
KW Monoclonal antibody; human; Hu19C; engineered antibody; RSV;
KW respiratory syncytial virus; complementarity determining region;
KW CDR; infection; immunotherapy; therapy; diagnosis; Hu19CHcpd; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 13..1419
FT mutation /*tag= a
FT /*tag= b
FT /note= "alters codon TCA (Ser) to GCA (Ala)"
XX
PN WO9819704-A1.
XX
PD 14-MAY-1998.
XX
PF 23-OCT-1997; 97WO-US19203.
XX
PR 01-NOV-1996; 96US-0030149.
XX
PA (SMK ) SMITHKLINE BEECHAM CORP.
XX
PI Deen KC, Dillon SB, Porter TG, Sweet RW;
XX
DR WPI; 1998-286600/25.
XX
DR P-PSDB; AAW59625, AAW59628 and AAW59631.
XX
PT Monoclonal antibodies reactive with Respiratory Syncytial Virus -
XX useful for detection, prevention and treatment of RSV infections
XX
PS Example C; Fig 4B; 109pp; English.
XX
CC This is the DNA sequence of plasmid Hu19CHcpd, which includes a
CC coding region for anti-respiratory syncytial virus (RSV) fusion
CC (F) protein human monoclonal antibody (MAB) Hu19C heavy chain (see
CC also AAW59617). Hu19CHcpn (see AAV41433) encoding the Hu19C light
CC chain is also provided. These vectors were used to produce Hu19C
CC in transfected COS and CHO cells. Hu19A, Hu19B, Hu19C and Hu19D
CC MABs are claimed. These are reshaped human antibodies comprising a
CC heavy chain selected from 19A, 19B, 19C or 19D (see AAW59615-18), and
CC a light chain selected from 19A, 19B, 19C or 19D (see AAW59620-21).
CC These are neutralising engineered antibodies that inhibit virus
CC growth in vitro and in vivo in animal models of RSV infection.
CC They can be used in the detection, prevention and passive
CC immunotherapy of RSV infection. Nucleic acids encoding the human
CC MABs, recombinant plasmids (see AAV41427-33) and host cells are
CC provided.
XX
SQ Sequence 1427 BP; 325 A; 461 C; 383 G; 258 T; 0 other;
```

```
Query Match 85.5%; Score 1141.8; DB 19; Length 1427;
Best Local Similarity 91.6%; Pred. No. 1.4e-213;
Matches 1241; Conservative 0; Mismatches 87; Indels 27; Gaps 2;
QY 2 AGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
Db 71 AGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 130
QY 62 CCTGTGCAGCTAGCGGATTCACCTTTCAGTGGCTACTGGTCTCTGGTCCGCCAGGCTC 121
Db 131 CGTGTGCAGCCTCTGGAAACCAACCCCTCAGTGGCTATACCATGCTGGTCCGCCAGGCTC 190
QY 122 CAGGAAGGGGCTCGAGTGGGTGCTGAAATCTAGATTGAAATCTGATAATTTATCAACAC 181
Db 191 CAGGAAGGGGCTCGAGTGGGTGCTGATCCATT-----ACTGGAGGTAGCAACTTCATAA 244
```

QY	182	ATTATCGGGAGTGTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC	241
Db	245	ACTACGCAGACTCAGTGAAGGGCGGATTTCACCATCTCCAGACACACGCCAACTCAC	304
QY	242	TGTATCTGCAAAATGAACAGCCTGAAACACGAGGACACACCGTGTATTACTGT-----	294
Db	305	TTTATCTGCAAAATGAACAGCCTGACAGCGAGACACACCGCTGTCTATTATTGTGCGACCG	364
QY	295	-----ACAGATTTTCATAGACTGGGGCAGGGAACACTAGTCACCGTCTCCT	340
Db	365	CCCTATAGCACCGCCCTACTTTTGACCACTGGGGCAGGAACCTGGTCAACGCTCTCT	424
QY	341	CAGCTCCACCAAGGGCCCATCGGTCTTCGCCCTGGCACCTCTCCAGAGCACTCTG	400
Db	425	CAGCTCCACCAAGGGCCCATCGGTCTTCGCCCTGGCACCTCTCCAGAGCACTCTG	484
QY	401	GGGGCACAGGGCCCTGGGGTGCTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTGT	460
Db	485	GGGGCACAGGGCCCTGGGGTGCTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTGT	544
QY	461	CGTGGAACTCAGCGGCCCTGACAGGGGGTGCACACCTTCCCGGCTGTCTTACAGTCTCT	520
Db	545	CGTGGAACTCAGCGGCCCTGACAGGGGGTGCACACCTTCCCGGCTGTCTTACAGTCTCT	604
QY	521	CAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCAACCCAGA	580
Db	605	CAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCAACCCAGA	664
QY	581	CCTACATCTGCAACGTGAATCAAGACCCAGCAACACCAAGGTGACAAAGATGGAGC	640
Db	665	CCTACATCTGCAACGTGAATCAAGACCCAGCAACACCAAGGTGACAAAGATGGAGC	724
QY	641	CCAAATCTTGTGACAAACTCACATGCCACCGTGCACAGCACCCTGAATCTCGGGGGG	700
Db	725	CCAAATCTTGTGACAAACTCACATGCCACCGTGCACAGCACCCTGAATCTCGGGGGG	784
QY	701	CACCGTCACTTCTCTTCCCCCAAAACCCAAAGGACACCCCTCATGATCTCCCGGACCC	760
Db	785	GACCGTCACTTCTCTTCCCCCAAAACCCAAAGGACACCCCTCATGATCTCCCGGACCC	844
QY	761	CTGAGTGCACATCGTGTGTGGAGCTGAGCCAGAGACCCCTGAGTCAAGTTCAACT	820
Db	845	CTGAGTGCACATCGTGTGTGGAGCTGAGCCAGAGACCCCTGAGTCAAGTTCAACT	904
QY	821	GGTACGTGACCGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACA	880
Db	905	GGTACGTGACCGCGTGGAGGTGCATAATGCCAAGACAAAGCCGGGAGGAGCAGTACA	964
QY	881	ACAGCAGTACCGTGTGGTCAAGCTCTTCCAAAGCCCTCCAGCCCCCATCGAGAAACCATCT	940
Db	965	ACAGCAGTACCGTGTGGTCAAGCTCTTCCAAAGCCCTCCAGCCCCCATCGAGAAACCATCT	1024
QY	941	AGGAGTACAAGTCCAAGGTCTCCAAAGCCCTCCAGCCCCCATCGAGAAACCATCT	1000
Db	1025	AGGAGTACAAGTCCAAGGTCTCCAAAGCCCTCCAGCCCCCATCGAGAAACCATCT	1084
QY	1001	CCAAAGCCAAAGGGCAGCCCCGAGAACCCACAGGTGTACACCTTCCCCCATCCCGGGATG	1060
Db	1085	CCAAAGCCAAAGGGCAGCCCCGAGAACCCACAGGTGTACACCTTCCCCCATCCCGGGATG	1144
QY	1061	AGCTGACCAAGAACAGGTGACCGTGAACCTGCCCTGGTCAAAGGCTTCTATCCCCAGCACA	1120
Db	1145	AGCTGACCAAGAACAGGTGACCGTGAACCTGCCCTGGTCAAAGGCTTCTATCCCCAGCACA	1204
QY	1121	TGCGCGTGGAGTGGGAGAGCAATGGGCAACCGGGAGAACAACTACAAGACCAACGCTCCCG	1180
Db	1205	TGCGCGTGGAGTGGGAGAGCAATGGGCAACCGGGAGAACAACTACAAGACCAACGCTCCCG	1264
QY	1181	TGCTGACCTCCAGCGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAAGCAGAGT	1240
Db	1265	TGCTGACCTCCAGCGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAAGCAGAGT	1324

QY	1241	GGCAGCAGGGAGACGCTTCTTCATGCTCCCGTGATGCATGAGGCTCTGCACAACCACTACA	1300
Db	1325	GGCAGCAGGGAGACGCTTCTTCATGCTCCCGTGATGCATGAGGCTCTGCACAACCACTACA	1384
QY	1301	CGCAGAGAGCGCTTCCTCGTCTCCGGGTAAATGA	1335
Db	1385	CGCAGAGAGCGCTTCCTCGTCTCCGGGTAAATGA	1419
RESULT	13		
AAV41432			
ID	AAV41432	standard; DNA; 1427 BP.	
XX			
AC	AAV41432;		
XX			
DT	12-OCT-1998	(first entry)	
XX			
DE	Plasmid Hui19DHcpd	encoding anti-RSV F protein Hui19D heavy chain.	
XX			
KW	Monoclonal antibody; human; Hui19D;	engineered antibody; RSV;	
KW	respiratory syncytial virus;	complementarity determining region;	
KW	CDR; infection; immunotherapy;	therapy; diagnosis; Hui19DHcpd; ss.	
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	13..1419	i
FT		/*tag= a	
FT	mutation	244	
FT		/*tag= b	
FT		/note= "alters codon AAC (Asn) to CAA (Gln)"	
FT	mutation	246	
FT		/*tag= c	
FT		/note= "alters codon AAC (Asn) to CAA (Gln)"	
XX			
PN	W09819704-A1.		
XX			
PD	14-MAY-1998.		
XX			
PF	23-OCT-1997;	97WO-US19203.	
XX			
PR	01-NOV-1996;	96US-0030149.	
XX			
PA	(SMIK) SMITHKLINE BEECHAM CORP.		
PI	Deen KC, Dillion SB, Porter TG, Sweet RW;		
XX			
PI	WPI: 1998-286600/25.		
DR	P-PSDB; AAW59625, AAW59628 and AAW59632.		
XX			
PT	Monoclonal antibodies reactive with Respiratory Syncytial Virus -		
PT	useful for detection, prevention and treatment of RSV infections		
XX			
PS	Example C; Fig 4F; 109pp; English.		
XX			
CC	This is the DNA sequence of plasmid Hui19DHcpd, which includes a		
CC	coding region for anti-respiratory syncytial virus (RSV) fusion		
CC	(F) protein human monoclonal antibody (MAB) Hui19D heavy chain (see		
CC	also AAW59618). Hui19C1cpn (see AAV41433) encoding the Hui19C light		
CC	chain is also provided. These vectors were used to produce Hui19C		
CC	in transfected COS and CHO cells. Hui19A, Hui19B, Hui19C and Hui19D		
CC	MABs are claimed. These are reshaped human antibodies comprising a		
CC	heavy chain selected from 19A, 19B, 19C or 19D (see AAW59615-18), and		
CC	a light chain selected from 19A, 19B, 19C or 19D (see AAW59620-21).		
CC	These are neutralising engineered antibodies that inhibit virus		
CC	growth in vitro and in vivo in animal models of RSV infection.		
CC	They can be used in the detection, prevention and passive		
CC	immunotherapy of RSV infection. Nucleic acids encoding the human		
CC	MABs, recombinant plasmids (see AAV41427-33) and host cells are		
CC	provided.		
XX			
SQ	Sequence 1427 BP; 325 A; 461 C; 382 G; 259 T; 0 other:		

Query Match 85.5%; Score 1141.8; DB 19; Length 1427;
Best Local Similarity 91.6%; Pred. No. 1.4e-213;
Matches 1241; Conservative 0; Mismatches 87; Indels 27; Gaps 2;

Qy 2 AGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGGTCCCTTAGACTCT 61
Db 71 AGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGGTCCCTTAGACTCT 130
Qy 62 CTTGTGACGCTAGCGGATTCATTTTCAGTGGCTACTGGATGCTCTGGTCCGCCAGGCTC 121
Db 131 CTTGTGACGCTAGCGGATTCATTTTCAGTGGCTACTGGATGCTCTGGTCCGCCAGGCTC 190
Qy 122 CAGGGAAGGGCTCGAGTGGTCTGCTGAAATTTAGATTTGAAATCTGATAATATGCAACAC 181
Db 191 CAGGGAAGGGCTCGAGTGGTCTGCTGAAATTTAGATTTGAAATCTGATAATATGCAACAC 244
Qy 182 ATTAGCGGAGTCTGTGAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 241
Db 245 AATAGTCAAGTCTAGTGAAGGGCGGATTCACCATCTCAAGAGATGATTCAAAATCTAGAC 304
Qy 242 TGTATCTCAAAATGAACAGCCTGAAAACCGAGGACACAGCGGTGTATTACTGT----- 294
Db 305 TTTATCTCAAAATGAACAGCCTGACGCGGAGGACAGCGGTGTATTATTGTGCGACCG 364
Qy 295 -----ACAGATTTTCATAGACTGGGGCCAGGGAACTAGTCAACGCTCTCCT 340
Db 365 CCCCTATAGCACCGCCCTACTTTGACCACCTGGGGCCAGGAAACCCCTGTCACCGCTCTCCT 424
Qy 341 CAGCCTCCACCAAGGGCCCATCGTCTTCCCGCTGGGACCTCTCTCCAAAGAGCACCTCTG 400
Db 425 CAGCCTCCACCAAGGGCCCATCGTCTTCCCGCTGGGACCTCTCTCCAAAGAGCACCTCTG 484
Qy 401 GGGGCACAGCGCCCTGGGCTCGCTGTGTCACAGGACTACTTCCCGAACCGGTGACGGTGT 460
Db 485 GGGGCACAGCGCCCTGGGCTCGCTGTGTCACAGGACTACTTCCCGAACCGGTGACGGTGT 544
Qy 461 CGTGAATCTCAGGCGCCCTGACAGCGCGGTGACACCTTCCCGGCTGTCTCAGTCTCT 520
Db 545 CGTGAATCTCAGGCGCCCTGACAGCGCGGTGACACCTTCCCGGCTGTCTCAGTCTCT 604
Qy 521 CAGGACTCTACTCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGACCCGAGA 580
Db 605 CAGGACTCTACTCTCAGCAGCGTGGTGACCGTGCCTCCAGCAGCTTGGGACCCGAGA 664
Qy 581 CTTACATCTGCAAGTGAATCACAAGCCCAAGCAACACCAAGGTGGACAAAGAAAGTGAGC 640
Db 665 CTTACATCTGCAAGTGAATCACAAGCCCAAGCAACACCAAGGTGGACAAAGAAAGTGAGC 724
Qy 641 CCAATCTTGTGACAAAATCTACACATGCCACCGTGCCCGACGACCTGAACCTCGCGGGG 700
Db 725 CCAATCTTGTGACAAAATCTACACATGCCACCGTGCCCGACGACCTGAACCTCGCGGGG 784
Qy 701 CACCCTCAGTCTCTCTTCTTCCCGCCAAACCAAGGACACCCCTCATGATCTCCCGGACCC 760
Db 785 GACCGTCACTCTCTCTTCTTCCCGCCAAACCAAGGACACCCCTCATGATCTCCCGGACCC 844
Qy 761 CTGAGGTCAATGCTGTGTGTGACGTGACGACGACCAAGACCCCTGAGTCAAGTTCAACT 820
Db 845 CTGAGGTCAATGCTGTGTGTGACGTGACGACGACCAAGACCCCTGAGTCAAGTTCAACT 904
Qy 821 GGTACGTGAGCGGCTGTGAGTGTGATATGCAAGACAAAGCCCGGAGGAGCAGTACA 880
Db 905 GGTACGTGAGCGGCTGTGAGTGTGATATGCAAGACAAAGCCCGGAGGAGCAGTACA 964
Qy 881 ACAGCACGTACCGTGTGTCAGCGCTCTCACCCTGCTGACCCAGGACTGGCTGAATGGCA 940
Db 965 ACAGCACGTACCGGCTGTGTCAGCGCTCTCACCCTGCTGACCCAGGACTGGCTGAATGGCA 1024
Qy 941 AGGAGTACAGTGCAGGCTCTCCACAAAGCCCTCCAGCCGCCCATCGAGAAAACCATCT 1000
Db 1025 AGGAGTACAGTGCAGGCTCTCCACAAAGCCCTCCAGCCGCCCATCGAGAAAACCATCT 1084

Qy 1001 CCAAAAGCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCCCCATCCCCGGGATG 1060
Db 1085 CCAAAAGCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCCCCATCCCCGGGATG 1144
Qy 1061 AGCTGACCAAGAACAGGTCAGCCTGACCTGCTGTGTCAAAGGCTTCTATCCACGCGACA 1120
Db 1145 AGCTGACCAAGAACAGGTCAGCCTGACCTGCTGTGTCAAAGGCTTCTATCCACGCGACA 1204
Qy 1121 TCGCCCTGGAGTGGGAGAGCAATGGGACGCCGAGAACAACTACAGACCCAGCCCTCCCG 1180
Db 1205 TCGCCCTGGAGTGGGAGAGCAATGGGACGCCGAGAACAACTACAGACCCAGCCCTCCCG 1264
Qy 1181 TGTGACTCCGACGGCTCCTTCTTCCTTACAGACAGCTACCGTGGACACAGCAGGT 1240
Db 1265 TGTGACTCCGACGGCTCCTTCTTCTTACAGCAAGCTACCGTGGACACAGCAGGT 1324
Qy 1241 GGCAGCAGGGGAGCGTCTTCTCATGCTCGTGTATGATGAGGCTCTGCAACAACCTACAC 1300
Db 1325 GGCAGCAGGGGAGCGTCTTCTCATGCTCGTGTATGATGAGGCTCTGCAACAACCTACAC 1384
Qy 1301 CGCAGAAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1335
Db 1385 CGCAGAAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1419
RESULT 14
AAV41429
ID AAV41429 standard; DNA; 1427 BP.
XX
AC AAV41429;
XX
DT 12-OCT-1998 (first entry)
XX
DE Plasmid Hu19BHcpd encoding anti-RSV F protein Hu19B heavy chain.
XX
KW Monoclonal antibody; human; Hu19B; engineered antibody; RSV;
KW respiratory syncytial virus; complementarity determining region;
KW CDR; infection; immunotherapy; therapy; diagnosis; Hu19BHcpd; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 13..1419
FT /*tag= a
XX
PN WO9819704-A1.
XX
PD 14-MAY-1998.
XX
PF 23-OCT-1997; 97WO-US19203.
XX
PR 01-NOV-1996; 96US-0030149.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Deen KC, Dillon SB, Porter TG, Sweet RW;
XX
DR WPI; 1998-286600/25.
DR P-PSDB; AAW59625 and AAW59628.
XX
PT Monoclonal antibodies reactive with Respiratory Syncytial Virus -
PS useful for detection, prevention and treatment of RSV infections
XX
PS Example B; Fig 4C; 109pp; English.
XX
CC This is the DNA sequence of plasmid Hu19BHcpd, which includes a
CC coding region for anti-respiratory syncytial virus (RSV) fusion
CC (F) protein human monoclonal antibody (MAb) Hu19B heavy chain (see
CC also AAW59616). Hu19BLcpn (see AAV41430) encoding the Hu19B light
CC chain is also provided. These vectors were used to produce Hu19B
CC in transfected COS and CHO cells. Hu19A, Hu19B, Hu19C and Hu19D
CC MAbs are claimed. These are reshaped human antibodies comprising a
CC heavy chain selected from 19A, 19B, 19C or 19D (see AAW59615-18), and

a light chain selected from 19A, 19B, 19C or 19D (see AAW59620-21). These are neutralising engineered antibodies that inhibit virus growth *in vitro* and *in vivo* in animal models of RSV infection. They can be used in the detection, prevention and passive immunotherapy of RSV infection. Nucleic acids encoding the human MAb, recombinant plasmids (see AAV1427-33) and host cells are provided.

SQ Sequence 1427 BP; 325 A; 461 C; 382 G; 259 T; 0 other;

Query Match 85.4%; Score 1140.2; DB 19; Length 1427;
Best Local Similarity 91.5%; Pred. NO. 2.9e-213;
Matches 1240; Conservative 0; Mismatches 88; Indels 27; Gaps 2;

QY	2	AGGTGCAGCTGGTGGAGCTGCGGGGAGCGTGTGTAAGCCCGGGGGTCCCTTTAGACTCT	61
Db			
Db	71	AGGTGCAGCTGGTGGAGCTGCGGGGAGCGTGTGTAAGCCCGGGGGTCCCTTTAGACTCT	130
QY	62	CCGTGTGAGCTAGCGGATTCACCTTTTCAGTGGCTACTGGATGTCTCTGGGTCCGCCAGCGTC	121
Db			
Db	131	CGTGTGAGCCTCTGGNACCACCCTCAGTGGCTATACCATGCACTGGTCCGCCAGCGCT	190
QY	122	CAGGGAAGGGCGTCGAGTGGGTGCTGAATATGATTTGAATCTGATAATTATGCAACAC	181
Db			
Db	191	CAGGGAAGGGCGTCGAGTGGGTCTCATCCATT-----ACTGGAGTAGCAACTTCATATA	244
QY	182	ATTATGCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAATCTAGAC	241
Db			
Db	245	ACTACTCAGACTCAGTGAAGGGCGGATTCACCATCTCCAGAGACAAGCCGAAGAAGCTC	304
QY	242	TGTATCTGCAATGAACAGCGCTGAAACCGAGAGACACAGCCGTGTATTACTGT-----	294
Db			
Db	305	TTTATCTGCAATGAACAGCGCTCAGAGCGAGGACACGGCTGCTATTATTGTGGACCG	364
QY	295	-----ACAGATTTTCATAGACTGGGGCCAGGGAACACTAGTCAACGCTCTCT	340
Db			
Db	365	CCCTATAGCACCGCCCTACTTTGACACTGGGGCCAGGGAACCCCTGTCACCGTCTCT	424
QY	341	CAGCCTCCACCAAGGGCCCATCGGTCTTCCCTCTGCGACCCCTCTCCAAAGACGACCTCTG	400
Db			
Db	425	CAGCCTCCACCAAGGGCCCATCGGTCTTCCCTCTGCGACCCCTCTCCAAAGACGACCTCTG	484
QY	401	GGGGCACAGCGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGT	460
Db			
Db	485	GGGGCACAGCGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGGAACCGGTGACCGTGT	544
QY	461	CGTGGAACTCAGCGGCCCTGACACAGCGGGGTGCACACCTTCCCGGTGCTCTACAGTCT	520
Db			
Db	545	CGTGGAACTCAGCGGCCCTGACACAGCGGGGTGCACACCTTCCCGGTGCTCTACAGTCT	604
QY	521	CAGGACTCTACTCCCTCAGCAGGGTGGTGACCGTGGCCCTCCAGCAGCTTGGGGACCCAGA	580
Db			
Db	605	CAGGACTCTACTCCCTCAGCAGGGTGGTGACCGTGGCCCTCCAGCAGCTTGGGGACCCAGA	664
QY	581	CCTACATCTGCAACGTGAATCACAGCCAGCAACACCAAGGTGGACAAGAAGTGGAGC	640
Db			
Db	665	CCTACATCTGCAACGTGAATCACAGCCAGCAACACCAAGGTGGACAAGAAGTGGAGC	724
QY	641	CCAATCTTGTGACAAACTCACATGATGCCCCCGTGGCCAGCACTGAAGCTCGGGGG	700
Db			
Db	725	CCAAATCTTGTGACAAACTCACATGATGCCCCCGTGGCCAGCACTGAAGCTCGGGGG	784
QY	701	CACGGTCAGTCTCTCTTCCCCCAAAACCCCAAGGACACCCCTCATGATCTCCCGGACCC	760
Db			
Db	785	GACCGTCAGTCTCTCTTCCCCCAAAACCCCAAGGACACCCCTCATGATCTCCCGGACCC	844
QY	761	CTGAGTGCATGCGTGGTGGAGCGTGAGCGCACGAAGACCCCTGAGGTCAAGTTTCAACT	820
Db			
Db	845	CTGAGTGCATGCGTGGTGGAGCGTGAGCGCACGAAGACCCCTGAGGTCAAGTTTCAACT	904
QY	821	GGTACGTGGAAGCGCGTGGAGGTGCATAATGCCAAGACAAGCCGGGGAGGAGCAGTACA	880
Db			
Db	905	GGTACGTGGAAGCGCGTGGAGGTGCATAATGCCAAGACAAGCCGGGGAGGAGCAGTACA	964

CC derived from a variety of human tissues. The invention also provides
CC a method for producing proteins from these polynucleotide sequences.
CC The proteins are useful for identifying compounds that modulate their
CC activity and production, and the cell is also useful for identifying
CC compounds that modulate expression of the polynucleotide sequences
CC encoding the secreted proteins. The sequences of the invention are
CC useful for treating diseases such as hyperproliferative disorders
CC (e.g. cancer), immune deficiency disorders (e.g. severe combined
CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
CC sclerosis), blood disorders (e.g. thrombocytopenia), inflammatory
CC disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).
CC The polynucleotide sequences of the invention are also useful in gene
CC therapy. AAS62214-AAS62838 represent the cDNA sequences of the
CC invention that encode for novel human secreted proteins

Sequence 1617 BP; 375 A; 507 C; 437 G; 298 T; 0 other;

Query Match 85.1%; Score 1136.6; DB 24; Length 1617;
Best Local Similarity 91.2%; Pred. No. 1.5e-212;
Matches 1240; Conservative 0; Mismatches 89; Indels 30; Gaps 2;

Qy	1	GAGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTTAGACTC	60
Db	123	GAGTGTGTTGTTGGAGTTCAGGGGAGGCTTGGTACAGCTCGAGGGTCCCTTGAGACTC	182
Qy	61	TCCTGTGCAGCTACGCGATTCACTTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCT	120
Db	183	TCCTGTGAGGCCTCTGGAATTCACCTTCAGTAGTTATGAAATGAATTGGGTCCGCCAGGCT	242
Qy	121	CCAGGGAAGGGGCTCGAGTGGGTTGCTGAAATTAGATTGAAATCTGATAATATTGCAACA	180
Db	243	CCAGGGAAGGGCTGGAGTGGTTCATACATCAGTCAGA-----CTGGTCTTGTTCATC	296
Qy	181	CATTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAAATCTAGA	240
Db	297	CAC'TACGACACTCTGTGAAGGGCCGATTCCACATTTCCAGAGACACGCCAAGAACTCA	356
Qy	241	CTGTATCTGCAAAATGACACGCTGAAAACCGAGAGACACGCCGTGTATTACTCTAC	296
Db	357	GTGTATCTGCAAAATGCACGCCTGAGAGCCGACGACACGGCTGTGTACTCTCTGGCGAGA	416
Qy	297	-----AGATTTCATAGACTGGGGCCAGGGAACACTAGTACCCCGTC	336
Db	417	TACCCGTTAGCAGCTGCTGGAACCTTTTGAACACTGGGGCCAGGGAACCCCGGTCAACGTC	476
Qy	337	TCCTCAGGCTCCACCAAGGGCCATCGGTCCTTCCCCCTGSCACCCCTCTCCAGAGACCC	396
Db	477	TCCTCAGCCTCCACCAAGGGCCATCGGTCCTTCCCCCTGGCACCCCTCTCCAGAGACCC	536
Qy	397	TCTGGGGGCACAGGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCGGTGACG	456
Db	537	TCTGGGGGCACAGGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCGGTGACG	596
Qy	457	GTGTCGTGGAACTCAGCGGCCCTGACCAAGCGGGGTGCACACCTTCCCGGCTGTCTTACAG	516
Db	597	GTGTCGTGGAACTCAGCGGCCCTGACCAAGCGGGGTGCACACCTTCCCGGCTGTCTTACAG	656
Qy	517	TCCTCAGAGCTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTTCCAGCAGCTTGGGGACC	576
Db	657	TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTTCCAGCAGCTTGGGCACC	716
Qy	577	CAGACCTACATCTGCAAGCTGAATCACAAGCCGAGCAACACCAAGTGGGACAGAAAGTG	636
Db	717	CAGACCTACATCTGCAAGCTGAATCACAAGCCGAGCAACACCAAGTGGGACAGAAAGTG	776
Qy	637	GAGCCCAAACTCTGTGACAAAACCTACACATGCCCACCGTGGCCAGCAACCTGAACTCGCG	696
Db	777	GAGCCCAAACTCTGTGACAAAACCTACACATGCCCACCGTGGCCAGCAACCTGAACTCGCG	836
Qy	697	GGGACACCGTCAGTCTTCTCTTCCCCCAAAACCCCAAGGACACCCCTCATGATCTCCCGG	756
Db	837	GGGACACCGTCAGTCTTCTCTTCCCCCAAAACCCCAAGGACACCCCTCATGATCTCCCGG	896

QY	757	ACCCCTGAGGTACATCGCTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTC	CAAGTTC	816
DB	897	ACCCCTGAGGTACATCGCTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTC	CAAGTTC	956
QY	817	AACTGGTACCTGGACGGCTGGAGGTGCAATAATCCAAAGCAAAAGCCGGGAGGACG	876	
DB	957	AACTGGTACCTGGACGGCTGGAGGTGCAATAATCCAAAGCAAAAGCCGGGAGGACG	1016	
QY	877	TACAACAGCAGCTACCGTGTGGTTCAGCGTCTCAACGCTCTGCACAGGACTGGCTGAAT	936	
DB	1017	TACAACAGCAGCTACCGTGTGGTTCAGCGTCTCAACGCTCTGCACAGGACTGGCTGAAT	1076	
QY	937	GGCAAGGAGTACAAGTGCAAGTCTCCAAACAAGCCCTCCACGCCCATCGAGAAACC	996	
DB	1077	GGCAAGGAGTACAAGTGCAAGTCTCCAAACAAGCCCTCCACGCCCATCGAGAAACC	1136	
QY	997	ATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTACACCTCGCCCATCCCGG	1056	
DB	1137	ATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTACACCTCGCCCATCCCGG	1196	
QY	1057	CATCAGCTGACCAAGAACCAGGTTCAGCCTGACCTGCTGGTCAAGAGCTTCTATCCCAGC	1116	
DB	1197	CATCAGCTGACCAAGAACCAGGTTCAGCCTGACCTGCTGGTCAAGAGCTTCTATCCCAGC	1256	
QY	1117	GACATCCCGTGGAGTGGGAGAGCAATAGGGCAGCCGGAGAACACTACAGACCAACGCT	1176	
DB	1257	GACATCCCGTGGAGTGGGAGAGCAATAGGGCAGCCGGAGAACACTACAGACCAACGCT	1316	
QY	1177	CCCGTGTGACCTCCGACGGCTCTTCTTCTCTACACCAAGCTCACCGTGGACAAGGC	1236	
DB	1317	CCCGTGTGACCTCCGACGGCTCTTCTTCTCTACACCAAGCTCACCGTGGACAAGGC	1376	
QY	1237	AGGTGGCAGCAGGGGAACGCTTCTTCATGCTCCGCTGATGCATGAGGCTCTGCACAACC	1296	
DB	1377	AGGTGGCAGCAGGGGAACGCTTCTTCATGCTCCGCTGATGCATGAGGCTCTGCACAACC	1436	
QY	1297	TACACGCAAGAGCCCTCTCCCTGTCTCCGGTAAATGA	1335	
DB	1437	TACACGCAAGAGCCCTCTCCCTGTCTCCGGTAAATGA	1475	

Search completed: April 26, 2003, 05:06:15
Job time : 294.58 secs

GenCore version 5.1.4_p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 07:27:07 ; Search time 129.024 Seconds
(without alignments)
11258.801 Million cell updates/sec

Title: US-09-674-716b-18
Perfect score: 1335
Sequence: 1 gaggtgacgtgtgagtc.....ccctgtctccgggtaaatga 1335

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 709820 seqs, 544064369 residues
Total number of hits satisfying chosen parameters: 1419640

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1147.8	86.0	1798	9 US-09-925-299-230	Sequence 230, App
2	1147.8	86.0	1798	10 US-09-925-299-230	Sequence 230, App
3	1147.2	85.9	1437	9 US-10-124-905-7	Sequence 7, Appli
4	1147.2	85.9	1437	9 US-09-948-429B-7	Sequence 7, Appli
5	1147.2	85.9	1437	9 US-10-073-138-4	Sequence 4, Appli
6	1145	85.8	1616	10 US-09-822-830A-572	Sequence 572, App
7	1141.8	85.5	1427	12 US-10-066-895-25	Sequence 25, Appl
8	1141.8	85.5	1427	12 US-10-066-895-27	Sequence 27, Appl
9	1140.2	85.4	1427	12 US-10-066-895-20	Sequence 20, Appl
10	1136.6	85.1	1617	10 US-09-822-830A-571	Sequence 571, App
11	1135	85.0	1347	10 US-09-736-371B-20	Sequence 20, Appl
12	1131	84.7	1356	10 US-09-822-698A-27	Sequence 27, Appl
13	1128.8	84.6	6284	12 US-10-066-895-14	Sequence 14, Appl
14	1121.4	84.0	9182	9 US-09-927-122-41	Sequence 41, Appl
15	1105.2	82.8	1598	10 US-09-822-849A-103	Sequence 103, App
16	1104.8	82.8	1404	10 US-09-825-012-10	Sequence 10, Appl
17	1102.2	82.6	2196	10 US-09-825-012-44	Sequence 44, Appl
18	1102.2	82.6	2196	10 US-09-825-012-45	Sequence 45, Appl
19	1102.2	82.6	2226	10 US-09-825-012-53	Sequence 53, Appl

20	1102.2	82.6	2226	10 US-09-825-012-54	Sequence 54, Appl
21	1100	82.4	1590	10 US-09-822-849A-114	Sequence 114, App
22	1096.6	82.1	2190	10 US-09-825-012-50	Sequence 50, Appl
23	1096.6	82.1	2190	10 US-09-825-012-51	Sequence 51, Appl
24	1096.6	82.1	2220	10 US-09-825-012-59	Sequence 59, Appl
25	1096.6	82.1	2220	10 US-09-825-012-60	Sequence 60, Appl
26	1095.8	82.1	2193	10 US-09-825-012-47	Sequence 47, Appl
27	1095.8	82.1	2193	10 US-09-825-012-48	Sequence 48, Appl
28	1095.8	82.1	2223	10 US-09-825-012-56	Sequence 56, Appl
29	1095.8	82.1	2223	10 US-09-825-012-57	Sequence 57, Appl
30	1088	81.5	3300	9 US-10-020-786-1	Sequence 1, Appli
31	1086	81.3	3300	9 US-10-020-786-2	Sequence 2, Appli
32	1082.6	81.1	8120	9 US-09-726-258-68	Sequence 68, Appl
33	1082	81.0	4207	10 US-09-897-006-4	Sequence 4, Appli
34	1082	81.0	5732	10 US-09-897-006-6	Sequence 6, Appli
35	1082	81.0	9183	10 US-09-897-006-7	Sequence 7, Appli
36	1077.6	80.7	1615	10 US-09-822-849A-111	Sequence 111, App
37	1075.8	80.6	1634	10 US-09-822-830A-303	Sequence 303, App
38	1073	80.4	1576	10 US-09-822-830A-507	Sequence 507, App
39	1067.8	80.0	1640	10 US-09-822-849A-321	Sequence 321, App
40	1064.4	79.7	4210	10 US-09-897-006-5	Sequence 5, Appli
41	1064	79.7	1565	10 US-09-822-849A-241	Sequence 241, App
42	1061.4	79.5	1643	10 US-09-822-830A-302	Sequence 302, App
43	1057.6	79.2	1565	10 US-09-822-849A-104	Sequence 104, App
44	1050.6	78.7	1449	10 US-09-747-669-1	Sequence 1, Appli
45	1050.6	78.7	1449	10 US-09-747-669-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-925-299-230
; Sequence 230, Application US/0925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 230
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (15)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (24)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (31)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (501)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1798)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-230

Query Match 86.0%; Score 1147.8; DB 9; Length 1798;

	Best Local Similarity	91.08%; Pred. No. 4e-311;	Matches 1245; Conservative	10; Mismatches	73; Indels	40; Gaps	2;
QY	2	AGGTGACGCTGGTGAGTCTGGGGAGGCTTGGTAAAGCCGGGGGGTCCCTTAGACTCT	61				
Db	206	AGGTGCAGCTGTTGAGTCTGGGGAGGCGTGGTCCAGCCTGGAGGTCCCTGAGACTCT	265				
QY	62	CTGTGACGCTAGCGGATTCATTTTCAGTGCCTACTGGATGTCTGGTCCGCCAGGCTC	121				
Db	266	CTGTGACGCTCTCGATTCACCTTCAGTAGTATGTCATGCATCGCTGGTCCGCCAGGCTC	325				
QY	122	CAGGGAAGGGCTCCAGTGGTGTCTGAAATAGATTGAAATCTGATTAATATGCAACAC	181				
Db	326	CAGGCNAGGGCTGAGTGGGTGGCAGTTATATATATATATATATATATATATATATAT	379				
QY	182	ATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGAC	241				
Db	380	ACTATGCAGACTCCGTGAAGGGCGGATTCACCATCTCCAGAGACAATTCAGAAACACGC	439				
QY	242	TGTATCTCAATGAACAGCCTGAAACCCGAGGACACAGCGCTGTTATTACTGTACAGATT	301				
Db	440	TGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTTATTACTGTGCGARAG	499				
QY	302	TCAT-----AGACTGGGGCCAGGAAACACTA	327				
Db	500	ANGTTACTATGTTTCGAAAGCATCTACTACTTTGACTCTGGGGCCAGGAAACMCTG	559				
QY	328	GTACACGCTCTCTAGCCTCCACCAAGGGCCCATCGTCTTCCCGTCGACACCTCCTCC	387				
Db	560	GTACACGCTCTCTAGCCTCCACCAAGGGCCCATCGTCTTCCCGTCGACACCTCCTCC	619				
QY	388	AAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGTCTCAAGSACTACTTCCCGCAA	447				
Db	620	AAGAGCACCTCTGGGGGCACAGCGCCCTGGGCTGCCTGTCTCAAGSACTACTTCCCGCAA	679				
QY	448	CCGGTGACGGTGTCTGGAACCTAGCGCCCTGACACGCGCTGACACACTTCCCGGCT	507				
Db	680	CCGGTGACGGTGTCTGGAACCTAGCGCCCTGACACGCGCTGACACACTTCCCGGCT	739				
QY	508	GTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGC	567				
Db	740	GTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGC	799				
QY	568	TTGGGACCCGACCTACATCTGTCAACGTGAATCACAAGCCACGACACCAAGGTGGAC	627				
Db	800	TTGGGACCCGACCTACATCTGTCAACGTGAATCACAAGCCACGACACCAAGGTGGAC	859				
QY	628	AAGAAAGTGAGGCCCAAACTTTGTGACAAAACCTCACACATGCCACCGTGCACAGCACCT	687				
Db	860	AAGAAAGTGAGGCCCAAACTTTGTGACAAAACCTCACACATGCCACCGTGCACAGCACCT	919				
QY	688	GAATCCGGGGGACCGTCAGTCTTCTCTTCCCGCCCAACCCAGGACACCTCATG	747				
Db	920	GAATCCGGGGGACCGTCAGTCTTCTCTTCCCGCCCAACCCAGGACACCTCATG	979				
QY	748	ATCTCCGGACCCCTGAGTTCACATCGTGTGGTGGAGCTGAGCCAGGAAGACCCCTGAG	807				
Db	980	ATCTCCGGACCCCTGAGTTCACATCGTGTGGTGGAGCTGAGCCAGGAAGACCCCTGAG	1039				
QY	808	GTCAAAGTTCAACTGGTACGTGGACGGCTGGAGGTGCATTAATGCCAAGCAAAAGCCGCG	867				
Db	1040	GTCAAAGTTCAACTGGTACGTGGACGGCTGGAGGTGCATTAATGCCAAGCAAAAGCCGCG	1099				
QY	868	GAGGACGAGTACAACAGCAGCTACCGTGTGTCAGGCTCTCACCGTCTGCACACGAGAC	927				
Db	1100	GAGGACGAGTACAACAGCAGCTACCGTGTGTCAGGCTCTCACCGTCTGCACACGAGAC	1159				
QY	928	TGGCTGAATGGCAAGAGTACAAGTCAAGTCTCCAAACAAAGCCCTCCAGCCCCCATC	987				
Db	1160	TGGCTGAATGGCAAGAGTACAAGTCAAGTCTCCAAACAAAGCCCTCCAGCCCCCATC	1219				
QY	988	GAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGTACACCTGCC	1047				

```

RESULT 2
US-09-925-299-230
; Sequence 230, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 230
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (15)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (24)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (31)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (501)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1798)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-230

```

```

Query Match      86.0%; Score 1147.8; DB 10; Length 1798;
Best Local Similarity 91.0%; Pred. No. 4e-311;
Matches 1245; Conservative 10; Mismatches 73; Indels 40; Gaps
2:
ay 2 AGGTGCAGCTGTGGAGTCTGGGGAGGCTTGTAAGCCCGGGGGTCCCTTAGACTCT 61
    |||||
ab 206 AGGTGCAGCTGTGGAGTCTGGGGAGGCGTGTCAGCTGGGAGTCCCTTGAGACTCT 265
    |||||
ay 62 CCTGTGCAGCTACGCGAATTCACATTTTCAGTGGGTACTGSGATGCTCGGGTCCGCCAGGCTC 121

```


QY 1 GAGGTGACGTGTTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 58 GAGGTGCAACTGGTGGAGTCTGGGGAGGCTTGGTCCAGCCTGGCGGTCCCTGAGAGTC 117
QY 61 TCCTGTGACAGTACGCGATTCACTTTCAGTGGTACTGGATGTCCTGGGTCCGCCAGGCT 120
Db 118 TCCTGTGACGTCTGTGATTCACTTTCAGTGGTACTGGATGTCCTGGGTCCGCCAGGCT 177
QY 121 CCAGGGAAGGGGTCGAGTGGTGGTGAATAGATTGAATGCTGTAATATGAACA 180
Db 178 CCAGGGAAGGGGTCGAGTGGTGGTGAATAGATTGAATGCTGTAATATGAACA 237
QY 181 CATTATCCGGAGTCTGTGAAGGGAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
Db 238 GAATACCGCGCTGTGTGAAGACAGATTCCACCATCTCCAGAGATGATTCCAAAGCATC 297
QY 241 CTGTATCTGCAATGAACAGCCTGGAACCCAGGACACACGCCGTGTATCTACTAC 296
Db 298 GCCTATCTGCAATGAGCAGCCTGAAATCGAGGACACGCCGTGTATCTACTACTACA 357
QY 297 -----AGATTTTCATAGACTGGGC 315
Db 358 TCCTACATTTTCACATTTGTCGGGGTGGTGTCTGCTATGAGGTTACTTCGAATTTCTGGGC 417
QY 316 CAGGGAACACTAGTACCGCTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTG 375
Db 418 CAGGGCGCCTGGTCAACCGTCTCCTCAGTACGACCAAGGGCCCATCGGTCTTCCCGCTG 477
QY 376 GCACCTCTCCAGAGCAGCTCTGGGGGACAGCGGCCCTGGCTGCTGGTCAAGGAC 435
Db 478 GCACCTCTCCAGAGCAGCTCTGGGGGACAGCGGCCCTGGCTGCTGGTCAAGGAC 537
QY 436 TACTTCCCGGAACCGGTGACGGTCTGTGGAACCTCAGGCGCCCTGACAGCGCGGTGCAC 495
Db 538 TACTTCCCGGAACCGGTGACGGTCTGTGGAACCTCAGGCGCCCTGACAGCGCGGTGCAC 597
QY 496 ACCTTCCCGGTCTCTCAGTCTCTCAGGACTCTACTCCCTCAGCAGCGGTGACCGTG 555
Db 598 ACCTTCCCGGTCTCTCAGTCTCTCAGGACTCTACTCCCTCAGCAGCGGTGACCGTG 657
QY 556 CCCTCCAGCAGCTTGGGCACCCAGACCTTACATCTGCAACGTGAATCAACAGCCCAAG 615
Db 658 CCCTCCAGCAGCTTGGGCACCCAGACCTTACATCTGCAACGTGAATCAACAGCCCAAG 717
QY 616 ACCAAGTGGACAAAGAGTGGACCCCAATCTTGTGACAAACTCACATGCCCAAG 675
Db 718 ACCAAGTGGACAAAGAGTGGACCCCAATCTTGTGACAAACTCACATGCCCAAG 777
QY 676 TGCCCGACAGCTGACCTGCGGGGGGACCGCTCAGTCTTCTTCCCGCCCAAAACCCAAAG 735
Db 778 TGCCCGACAGCTGACCTGCGGGGGGACCGCTCAGTCTTCTTCCCGCCCAAAACCCAAAG 837
QY 736 GACACCTCATGATCTCCCGGACCCCTCAGGTACATCTGCTGGTGGAGGTGAGCCAC 795
Db 838 GACACCTCATGATCTCCCGGACCCCTCAGGTACATCTGCTGGTGGAGGTGAGCCAC 897
QY 796 GAAGACCTGAGGTCAAGTTCACATGTTACGTGGACGCGGTGGAGGTGCATATGCCAAG 855
Db 898 GAAGACCTGAGGTCAAGTTCACATGTTACGTGGACGCGGTGGAGGTGCATATGCCAAG 957
QY 856 ACAAGACCGGGGAGGACAGCTACACAGCAGCTACCGTGTGGTCAAGCTCTCAGCGTC 915
Db 958 ACAAGACCGGGGAGGACAGCTACACAGCAGCTACCGTGTGGTCAAGCTCTCAGCGTC 1017
QY 916 CTGCAACAGGACTGCTGAATGGGAAGAGTACAAGTCAAGTCAAGTCTCAACAAAGCCCTC 975
Db 1018 CTGCAACAGGACTGCTGAATGGGAAGAGTACAAGTCAAGTCTCAACAAAGCCCTC 1077
QY 976 CCAGCCCGCATCGAGAAACCATCTCCAAAGCGGACGCCCGGAGAACACAGGTG 1035
Db 1078 CCAGCCCGCATCGAGAAACCATCTCCAAAGCGGACGCCCGGAGAACACAGGTG 1137
QY 1036 TACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACAGGTGAGCTGACCTGACCTGCTG 1095

Db 1138 TACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACAGGTGACCTGACCTGCTG 1197
QY 1096 GTCAAGGCTTCTATCCAGGACATCGCGTGGAGTGGGAGCAATGGCAGCCGAG 1155
Db 1198 GTCAAGGCTTCTATCCAGGACATCGCGTGGAGTGGGAGCAATGGCAGCCGAG 1257
QY 1156 AACAACTAACAGCACGCTCCCGTGTGGACTCCGACGCGCTCTTCTCTCTACAGC 1215
Db 1258 AACAACTAACAGCACGCTCCCGTGTGGACTCCGACGCGCTCTTCTCTCTACAGC 1317
QY 1216 AGCTCAGCGTGGACAAAGAGAGGTGGCAGCAGGGAACGCTTCTCATGCTCGGTGATG 1275
Db 1318 AAGCTCAGCGTGGACAAAGAGAGGTGGCAGCAGGGAACGCTTCTCATGCTCGGTGATG 1377
QY 1276 CATGAGGCTCTGCACAAACACTTACACGAGAGAGCCCTCTCCCTGCTCCGGTAAATGA 1335
Db 1378 CATGAGGCTCTGCACAAACACTTACACGAGAGAGCCCTCTCCCTGCTCCGGTAAATGA 1437

RESULT 4

US-09-948-429B-7
; Sequence 7, Application US/09948429B
; Patent No. US20020177689A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/948,429B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1437
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1437
US-09-948-429B-7

Query Match									
Best Local Similarity 85.9%; Score 1147.2; DB 9; Length 1437;									
Matches 1252; Conservative 90.7%; Pred No. 5.5e-311;									
Mismatches 0; Indels 45; Gaps 1;									
QY	1	GAGGTGACGCTGGTGGAGTCTGGGGAGCGTTGGTAAAGCCCGGGGGTCCCTTAGACTC	60						
DB	58	GAGGTGCAACTGGTGGAGTCTGGGGAGCGTTGGTCCAGCGTGGCGGGTCCCTGAGAGTC	117						
QY	61	TCTGTGACGCTAGCGATTCACTTTCAGTGGCTACTGGATCTCTGGTCCGCCAGGCT	120						
DB	118	TCTGTGACGCTCTGGATTCACTTTCAGTGGCTACTGGATCTCTGGTCCGCCAGGCT	177						
QY	121	CCAGGAAGGGGCTCGAGTGGTGGTGAATTTAGATTGAAATCTGATAATTTATCAACA	180						
DB	178	CCAGGAAGGGGCGGAATGGGTAGTTTCATTAGAAACAAACCGGTTGGGACACA	237						
QY	181	CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGA	240						
DB	238	GAATAGCGCGCTGTGTGAAGACAGATTCACCATCTCCAGAGATGATTCCAAAGCATC	297						
QY	241	CTGTATCTCAAAATGAACAGCCTGAAACCCGAGGACACAGCGCTGATTACTGTAC----	296						
DB	298	GCTATCTCAATGAGCAGCCTGAAATCGAGGACAGCGCGCTATTACTGTACTACA	357						
QY	297	-----AGATTTTCATAGACTGGGC	315						
DB	358	TCTACATTTTCAATTTGCGGGTGGTGTCTGCTATGGAGGTTACTTCGAATTTCTGGGC	417						
QY	316	CAGGGAACACTAGTACCGTCTCCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTG	375						
DB	418	CAGGCGCCCTGGTCAACGCTCTCCCTCAGCTAGCAGCAAGGGCCCATCGGTCTTCCCGCTG	477						
QY	376	GCACCTCTCTCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTGTCAGGAC	435						
DB	478	GCACCTCTCTCAAGAGCACCTCTGGGGCACAGCGCCCTGGGCTGCTGTGTCAGGAC	537						
QY	436	TACTTCCCGAACCGGTGACGGTGTCTGGAACTCAGCGGCCCTGACCAAGCGGTGAC	495						
DB	538	TACTTCCCGAACCGGTGACGGTGTCTGGAACTCAGCGGCCCTGACCAAGCGGTGAC	597						
QY	496	ACCTTCCCGGCTGCTCTCAGTCTCTCAGGACTTACTCCCTCAGCAGCGTGTGACCGTG	555						
DB	598	ACCTTCCCGGCTGCTCTCAGTCTCTCAGGACTTACTCCCTCAGCAGCGTGTGACCGTG	657						
QY	556	CCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTTGAATCAACGCCAGCAAC	615						
DB	658	CCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTTGAATCAACGCCAGCAAC	717						
QY	616	ACCAAGGTGGACAAGAGTGGAGCCCAATCTTGTGACAAACTCAGCATGCCACCG	675						
DB	718	ACCAAGGTGGACAAGAGTGGAGCCCAATCTTGTGACAAACTCAGCATGCCACCG	777						
QY	676	TGCCAGCACCTGAACTCGCGGGGACCGCTCAGTCTTCTTCCCGCCCAAAACCCCAAG	735						
DB	778	TGCCAGCACCTGAACTCTCTGGGGACCGCTCAGTCTTCTTCCCGCCCAAAACCCCAAG	837						
QY	736	GACACCTCTATGATCTCCCGGACCCCTGAGTTCACATCGTGGTGGAGCGTGGAGCCAC	795						
DB	838	GACACCTCTATGATCTCCCGGACCCCTGAGTTCACATCGTGGTGGAGCGTGGAGCCAC	897						
QY	796	GAAGACCTTGAGTCAAGTTCAACTGGTACGTGGAGCGCGTGGAGTGCATTAATGCCAAG	855						
DB	898	GAAGACCTTGAGTCAAGTTCAACTGGTACGTGGAGCGCGTGGAGTGCATTAATGCCAAG	957						
QY	856	ACAAAGCCGCGGAGGAGCAGTACAAACAGCAGTACCGTGGTGGTGGAGCGTCTCACCGTC	915						
DB	958	ACAAAGCCGCGGAGGAGCAGTACAAACAGCAGTACCGTGGTGGTGGAGCGTCTCACCGTC	1017						
QY	916	CTGCACACGAGCTGGCTGAATGGCAAGGAGTACAGTCAAGGTCTCCAAACAAAGCCCTC	975						
DB	1018	CTGCACACGAGCTGGCTGAATGGCAAGGAGTACAGTCAAGGTCTCCAAACAAAGCCCTC	1077						

QY	976	CCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCCAGAACACACAGGTG	1035
DB	1078	CCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCCAGAACACACAGGTG	1137
QY	1036	TACACCTTGCCTCCCATCCCGGATGAGCTACCAAGAACACAGGTACGCTGACCTGCGCTG	1095
DB	1138	TACACCTTGCCTCCCATCCCGGATGAGCTACCAAGAACACAGGTACGCTGACCTGCGCTG	1197
QY	1096	GTCAAGAGCTTCTATCCAGGAGCATCCCGTGGAGTGGAGAGCAATGGGAGCCGGAG	1155
DB	1198	GTCAAGAGCTTCTATCCAGGAGCATCCCGTGGAGTGGAGAGCAATGGGAGCCGGAG	1257
QY	1156	AACAACACAGAACACCGCTCCCGTGTGACTCCGACGCGCTCTTCTTCTCTACAGC	1215
DB	1258	AACAACACAGAACACCGCTCCCGTGTGACTCCGACGCGCTCTTCTTCTCTACAGC	1317
QY	1216	AAGCTACCGTGGACAAAGAGCAGGTGGCAGCGGGGAACTCTCTCATGCTCCGATG	1275
DB	1318	AAGCTACCGTGGACAAAGAGCAGGTGGCAGCGGGGAACTCTCTCATGCTCCGATG	1377
QY	1276	CATGAGCTCTGCAACACCACTACACGACAGAGCCTCTCCCTGTCTCCGGGTAAATGA	1335
DB	1378	CATGAGCTCTGCAACACCACTACACGACAGAGCCTCTCCCTGTCTCCGGGTAAATGA	1437

RESULT 5
US-10-073-138-4
; Sequence 4, Application US/10073138
; Publication No. US20020187146A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
; HANNA, Nabil
; BRAMS, Peter
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
; INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7
; AND B7.2 CO-STIMULATORY ANTIGENS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/073,138
; FILING DATE: 13-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/746,361
; FILING DATE: 08-NOV-1996
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1437 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:

```

; NAME/KEY: CDS
; LOCATION: 1..1437
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-073-138-4

Query Match      85.9%; Score 1147.2; DB 9; Length 1437;
Best Local Similarity 90.8%; Pred. No. 5.5e-311;
Matches 1252; Conservative 0; Mismatches 83; Indels 45; Gaps 1;

QY 1 GAGGTGACGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
DB 58 GAGGTGCAACTGGTGGAGTCTGGGGAGGCTTGGTCAGCGCTGGCGGGTCCCTGAGAGTC 117
QY 61 TCCTGTGACGCTAGCGGATTCACCTTTCCAGTGGCTACTGATGCTCCGCGCCAGGCT 120
DB 118 TCCTGTGACGCTCTGGATTACACCTTCAGTGACCACTACATGATTGGTTCCGCGCAGGCT 177
QY 121 CCAGGGAAGGGCTCGAGTGGTGGTGAATAGATTGAATCTGATTAATTAATGAACA 180
DB 178 CCAGGGAAGGGCGGAATGGGTAGGTTTCAATAGAAACCAACCGGCTGGGACAACA 237
QY 181 CATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
DB 238 GAATACGCCGCTGTGTGAAGACAGATTTCACCATCTCCAGAGATGATTCAAAAGCATC 297
QY 241 CTGTATCTGCAATGAACAGGCTGAAACCGGAGACACACCGGTGTATTACTGTAC---- 296
DB 298 GCCTATCTGCAATGAGCAGCCTGAAAATCGAGACACGCGCCTATTACTGTACTACA 357
QY 297 -----AGATTTTCATAGACTGGGC 315
DB 358 TCCTACATTTACAAATGTCGGGGTGGTGTCTGTATGAGAGGTACTTCGAAATTCGGGGC 417
QY 316 CAGGGAACACTAGTACCGCTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCGCCCTG 375
DB 418 CAGGGCGCCCTGGTCAACGCTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCGCCCTG 477
QY 376 GCACCTCTCTCAAGACGACCTCTGGGGGACACAGCGGCCCTGGGCTGCTTCAAGGAC 435
DB 478 GCACCTCTCTCAAGACGACCTCTGGGGGACACAGCGGCCCTGGGCTGCTTCAAGGAC 537
QY 436 TACTTCCCGCAACCGGTGACGCTGCTGTGAACCTCAAGCGCCCTGACACGCGCGTGCAC 495
DB 538 TACTTCCCGCAACCGGTGACGCTGCTGTGAACCTCAAGCGCCCTGACACGCGCGTGCAC 597
QY 496 ACCTTCCCGGCTGCTTACAGTCTCTCAGGACTCTACTTCCCTCAGCAGCGTGGTACCGTG 555
DB 598 ACCTTCCCGGCTGCTTACAGTCTCTCAGGACTCTACTTCCCTCAGCAGCGTGGTACCGTG 657
QY 556 CCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCGAGCAAC 615
DB 658 CCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCGAGCAAC 717
QY 616 ACCAAGTGGACAAAGAGTGGAGCCCAAAATCTTGTGACAAAACCTCACATGCCCCACCG 675
DB 718 ACCAAGTGGACAAAGAGAGAGCCCAAAATCTTGTGACAAAACCTCACATGCCCCACCG 777
QY 676 TGCCCGACCACTGAACTGCGGGGGGACCGGTCACTCTTCTTCCCGCCCAAAACCCAAAG 735
DB 778 TGCCCGACCACTGAACTGCGGGGGGACCGGTCACTCTTCTTCCCGCCCAAAACCCAAAG 837
QY 736 GACACCTTCATGATCTCCCGGACCCCTGAGGTACATCTGAGTGGTGGTGGAGTGGAGCCAC 795
DB 838 GACACCTTCATGATCTCCCGGACCCCTGAGGTACATCTGAGTGGTGGTGGAGTGGAGCCAC 897
QY 796 GAAGACCTCTGAGGTCAAGTTCACTGTTACGTGGACGCGCTGGAGGTGCATATGCGCAAG 855
DB 898 GAAGACCTCTGAGGTCAAGTTCACTGTTACGTGGACGCGCTGGAGGTGCATATGCGCAAG 957
QY 856 ACAAGCCCGGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTTCAGCGTCCCTACCGTC 915
DB 958 ACAAGCCCGGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTTCAGCGTCCCTACCGTC 1017
```

```

QY 916 CTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAAACAAAGCCCTC 975
DB 1018 CTGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAAACAAAGCCCTC 1077
QY 976 CCAGCCCCCATCGAGAAAACCATCTCCAAAGCAAAAGGCGAGCCCCGAGAACACACAGGTG 1035
DB 1078 CCAGCCCCCATCGAGAAAACCATCTCCAAAGCAAAAGGCGAGCCCCGAGAACACACAGGTG 1137
QY 1036 TACACCTCTGCCCCCATCCCGGGATGAGCTGACCAAGAACACACAGGTGACCTGACCTGCGCTG 1095
DB 1138 TACACCTCTGCCCCCATCCCGGGATGAGCTGACCAAGAACACACAGGTGACCTGACCTGCGCTG 1197
QY 1096 GTCAAAAGGCTTCTATCCAGCGACATCCCGCTGGAGTGGGAGAGCAATGGGACGCGGAG 1155
DB 1198 GTCAAAAGGCTTCTATCCAGCGACATCCCGCTGGAGTGGGAGAGCAATGGGACGCGGAG 1257
QY 1156 AACAACTCAACACACACGCGCTCCCGTGTGGACTCCGACGGCTCTTCTCTCTACAGC 1215
DB 1258 AACAACTCAACACACACGCGCTCCCGTGTGGACTCCGACGGCTCTTCTCTCTACAGC 1317
QY 1216 AAGCTCACCGTGGCAAGACAGAGTGGGACGAGGAGGAAACGTCTTCTCATGTCTCCGTGATG 1275
DB 1318 AAGCTCACCGTGGCAAGACAGAGTGGGACGAGGAGGAAACGTCTTCTCATGTCTCCGTGATG 1377
QY 1276 CATGAGGCTCTGCACACACCACTACAGCAGAGAGCGCTCTCCCTGTCTCCGGGTAAATGA 1335
DB 1378 CATGAGGCTCTGCACACCACTACAGCAGAGAGCGCTCTCCCTGTCTCCGGGTAAATGA 1437
```

```

RESULT 6
US-09-822-830A-572
; Sequence 572, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakr
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 572
; LENGTH: 1616
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1326,1377,1440,1579,1580
; OTHER INFORMATION: n=a,c,g, or t
US-09-822-830A-572
```

```

Query Match      85.8%; Score 1145; DB 10; Length 1616;
Best Local Similarity 90.8%; Pred. No. 2.3e-310;
Matches 1242; Conservative 0; Mismatches 93; Indels 33; Gaps 1;

QY 1 GAGGTGACGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTC'60
DB 123 GAGGTGACGCTGGTGGAGTCTGGGGAGGCTTGTATACAAACACGAGCGGTCCCTGAGACTC 182
QY 61 TCCTGTGACGCTAGCGGATTCACCTTCACTGGCTACTGGATCTCTGGTCCGCCAGGCT 120
DB 183 TCCTGTGACGAGGTTCGTGATTCCTGTTGGTGTGATTTGGTGTGAGCTGGGTCCGCCAGGCT 242
```

QY 121 CCAGGGAAGGGCTCGAGTGGTCTGTAATTTAGATTGAAATCTGATAATTATGCAACA 180
DB 243 CCAGGGAAGGGCTCGAGTGGTCTGTAATTTAGATTGAAATCTGATAATTATGCAACA 302
QY 181 CATTATCGGAGTCTGTGAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
DB 303 AATTACGGCGCTGTGTGACGGGAGATTCACCATCTCAAGAGATGATTCAAAAGCCATC 362
QY 241 CTGTATCTCAATGAACAGCTGAAACCGAGGACACAGCCGTGTTACTGTATA----- 295
DB 363 GCCTATCTGCAGATGAGCAGCTGAAACCGAGGACACAGCCCTTATCACTGTAGTAAA 422
QY 296 -----CAGATTTTCATAGACTGGGCGGCGAGGGAACACTA 327
DB 423 CATTACTATGATGATACTGGTTATCAGCAATACTTCCAACACTGGGCGGAGGCGACCGTG 482
QY 328 GTCACCGTCTCTCAGCTCCACCAAGGCGCATCTGGTCTTCCCGCTGGCAGCCCTCTCC 387
DB 483 GTCATCTCTCTCAGCTCCACCAAGGCGCATCTGGTCTTCCCGCTGGCAGCCCTCTCC 542
QY 388 AAGAGCACCCTCTGGGGGACAGCGGCCCTGGGCTGCTGCTGCTCAAGGACTACTTCCCGAA 447
DB 543 AAGAGCACCCTCTGGGGGACAGCGGCCCTGGGCTGCTGCTGCTCAAGGACTACTTCCCGAA 602
QY 448 CGGTGACGGTGTCTGTGAACCTCAGCGCCCTGTGACAGCGCGTGCACACCTTCCCGCT 507
DB 603 CGGTGACGGTGTCTGTGAACCTCAGCGCCCTGTGACAGCGCGTGCACACCTTCCCGCT 662
QY 508 GTCCTACAGTCTCAGGACTCTACTCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGC 567
DB 663 GTCCTACAGTCTCAGGACTCTACTCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGC 722
QY 568 TTGGGACCCAGACCTTACATCTGCAAGCTGAATCAAGCCCGCAGCAACCAAGGTTGAC 627
DB 723 TTGGGACCCAGACCTTACATCTGCAAGCTGAATCAAGCCCGCAGCAACCAAGGTTGAC 782
QY 628 AAGAAAGTGAGGCCAAATCTTGTGACAAACTCAGATGCCACCGTGCCTCCAGCAGCCT 687
DB 783 AAGAGAGTTGAGGCCAAATCTTGTGACAAACTCAGATGCCACCGTGCCTCCAGCAGCCT 842
QY 688 GAATCGGGGGGACCGCTCAGTCTTCTCTTCCCGCCCAAAACCAAGCAGCAGCCTCATG 747
DB 843 GAATCGTGGGGACCGCTCAGTCTTCTCTTCCCGCCCAAAACCAAGCAGCAGCCTCATG 902
QY 748 ATCTCCCGGACCCCTGAGTGCATCTGCTGTGGTGGAGTGGAGCCAGCAAGCCCTGAG 807
DB 903 ATCTCCCGGACCCCTGAGTGCATCTGCTGTGGTGGAGTGGAGCCAGCAAGCCCTGAG 962
QY 808 GTCAAGTTCAACTGTGTGACGCGCTGGAGTGCATATATGCCAAGCAAAAGCCGCGG 867
DB 963 GTCAAGTTCAACTGTGTGACGCGCTGGAGTGCATATATGCCAAGCAAAAGCCGCGG 1022
QY 868 GAGGAGCAGTACACAGCAGCTACCGTGTGTCAGCGTCTCAGCGTCTGCACACAGGAC 927
DB 1023 GAGGAGCAGTACACAGCAGCTACCGTGTGTCAGCGTCTCAGCGTCTGCACACAGGAC 1082
QY 928 TGCTGAATGCGAGAGTACAGTGCAGAGTCTCCACAAGCCCTCCAGCCCGCCATC 987
DB 1083 TGCTGAATGCGAGAGTACAGTGCAGAGTCTCCACAAGCCCTCCAGCCCGCCATC 1142
QY 988 GAGAAACCAATCTTCCAAAGCCAGGCGCCGAGAACCCAGAGTGTACACCTGTGCC 1047
DB 1143 GAGAAACCAATCTTCCAAAGCCAGGCGCCGAGAACCCAGAGTGTACACCTGTGCC 1202
QY 1048 CCATCCCGGATGAGTGCACCAAGACAGGTCAGCGTACCTGCTGGTCAAGGCTTC 1107
DB 1203 CCATCCCGGAGGATGATGACCAAGAACCCAGGTCAGCGTACCTGCTGGTCAAGGCTTC 1262
QY 1108 TATCCAGCAGCATCGCGTGGAGTGGAGAGCAATGCGAGCGGAGCAACCAACTACAG 1167
DB 1263 TATCCAGCAGCATCGCGTGGAGTGGAGAGCAATGCGAGCGGAGCAACCAACTACAG 1322
QY 1168 ACCACGCTTCCCGTGTGGACTCCGAGCGGCTCTTCTTCTCTACAGCAAGTCAACGCTG 1227

DB 1323 ACCNCGCTCCCGTCTGGACTCCGACGGTCTTCTCTCTATACCAAGCTCNCCTG 1382
QY 1228 GACAAGACAGGTGCGACAGGGAAGCTCTCTCATGCTCCGTCGATGATGAGGCTCTG 1287
DB 1383 GACAAGACAGGTGCGACAGGGAAGCTCTCTCATGCTCCGTCGATGATGAGGCTNTG 1442
QY 1288 CACAACCACTACACGACAGAAGGCTCTCCCTGTCTCCGGGTAATGA 1335
DB 1443 TTCAACCACTACACGACAGAAGGCTCTCCCTGTCTCCCGGTAATGA 1490

RESULT 7

US-10-066-895-25
; Sequence 25, Application US/10066895
; Patent No. US20020141990A1

GENERAL INFORMATION:

; APPLICANT: Deen, Keith C.
; Dillon, Susan B.
; Porter, Terence A.
; Sweet, Raymond A.

; TITLE OF INVENTION: Human Monoclonal Antibodies

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19046

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/066,895

; FILING DATE: 04-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 09/297,344

; FILING DATE: 1999-JUN-09

; APPLICATION NUMBER: 60/030,149

; FILING DATE: 01-NOV-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Gelger, Kathleen

; REGISTRATION NUMBER: 35,880

; REFERENCE/DOCKET NUMBER: P50504

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-5968

; TELEFAX: 610-270-5090

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1427 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-10-066-895-25

Query Match

Best Local Similarity: 91.6%; Score 1141.8; DB 12; Length 1427;

Matches 1241; Conservative 0; Mismatches 87; Indels 27; Gaps 2;

QY 2 AGGTGAGCTGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTCT 61

DB 71 AGGTGAGCTGTGGAGTCTGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTAGACTCT 130

QY 62 CCTGTGAGCTAGCGATTTCATTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCTC 121

DB 131 CGTGTGAGCTTGGAAACCAACCCCTCAGTGGCTATACCATGCACTGGGTCCGCCAGGCTC 190

QY	122	CAGGGAAGGGGCTCGAGTGGGTGCTGAAATTAGATTGAAATCTGATAATTTATGCAACAC	181
DB	191	CAGGGAAGGGGCTGGAGTGGGTCTCATCCATT-----ACTGGAGGTAGCAACTTCATAA	244
QY	182	ATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGAC	241
DB	245	ACTACTCAGACTCAGTGAAGGGCCGATTACCATCTCCAGAGACAACGCCAAGAACTCAC	304
QY	242	TGTATCTGCAAAATGAACAGCTGAAACACCGAGAGACACAGCCGTGTATTACTGT-----	294
DB	305	TTTATCTCAAAATGAACAGCTGACACGCGGAGACACGGCTGTATTATTGTGGGAACG	364
QY	295	-----ACAGATTTATAGACTGGGGCCAGGAAACACTAGTACACCGTCTCT	340
DB	365	CCCTATAGCACCGCCCTACTTTTGAACCACTGGGGCCAGGAAACCTGTGACCGTCTCT	424
QY	341	CAGCCTCCACCAAGGCCCATCGGTCTTCGCCCTGGCACCCCTCTCCAAAGACACCTGTG	400
DB	425	CAGCCTCCACCAAGGCCCATCGGTCTTCGCCCTGGCACCCCTCTCCAAAGACACCTGTG	484
QY	401	GGGGCACAGCGGCCCTGGGTGCTGTGAAGGACTACTTCCCGGAACCGGTGACGGTGT	460
DB	485	GGGGCACAGCGGCCCTGGGTGCTGTGAAGGACTACTTCCCGGAACCGGTGACCGTGT	544
QY	461	CGTGAACATCAGCGCCCTGACACAGCGCGTGCACACTTCCCGGGTGTCTACAGTCTCT	520
DB	545	CGTGAACATCAGCGGCCCTGACACAGCGCGTGCACACTTCCCGGGTGTCTACAGTCTCT	604
QY	521	CAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGAGCTTGGGGACCCAGA	580
DB	605	CAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGAGCTTGGGGACCCAGA	664
QY	581	CCTACATCTGCAACGTGAATCAAGCCCAAGCAACACCAAGGTGGACAAGAAAGTGGAGC	640
DB	665	CCTACATCTGCAACGTGAATCAAGCCCAAGCAACACCAAGGTGGACAAGAAAGTGGAGC	724
QY	641	CCAAATCTTTGACAAACTCAACATCCCAACCGTGCCCTCCAGAGCACTTGAAGTCCGGGGG	700
DB	725	CCAAATCTTTGACAAACTCAACATCCCAACCGTGCCCTCCAGAGCACTTGAAGTCCGGGGG	784
QY	701	CACCGTCAGTCTTCCTCTTCCCGCCCAAAACCCAAGGACACCCCTCATCATCTCCCGGACCC	760
DB	785	GACCGTCAGTCTTCTCTCTTCCCGCCCAAAACCCAAGGACACCCCTCATCATCTCCCGGACCC	844
QY	761	CTGAGGTCAATCGTGTGGTGTGAGCGTAGCGCAGAGACCCCTGAGGTCAAGTTCAACT	820
DB	845	CTGAGGTCAATCGTGTGGTGTGAGCGTAGCGCAGAGACCCCTGAGGTCAAGTTCAACT	904
QY	821	GGTACGTGAGCGCGTGGAGGTGCATATGCCAGACAAAACCGCGGAGGAGCAGTACA	880
DB	905	GGTACGTGAGCGCGTGGAGGTGCATATGCCAGACAAAACCGCGGAGGAGCAGTACA	964
QY	881	ACAGCAGTACCGTGTGGTCAAGCTCTCACCAANGCCCTCCAGCCAGGACTGGCTGAATGGCA	940
DB	965	ACAGCAGTACCGGGTGGTCAAGCTCTCACCAANGCCCTCCAGCCAGGACTGGCTGAATGGCA	1024
QY	941	AGGAGTACAAGTCAAGGTCTCCAACAANGCCCTCCAGCCAGGACTGGCTGAATGGCA	1000
DB	1025	AGGAGTACAAGTCAAGGTCTCCAACAANGCCCTCCAGCCAGGACTGGCTGAATGGCA	1084
QY	1001	CCAAGCCAAAGGCGACCCGAGAACCAAGGTGTACACCTGCCCCCATCCCGGGATG	1060
DB	1085	CCAAGCCAAAGGCGACCCGAGAACCAAGGTGTACACCTGCCCCCATCCCGGGATG	1144
QY	1061	AGTGTACCAAGAACCAAGGTGAGTGTGCTGGTCAAGGCTTCTATCCAGCGACA	1120
DB	1145	AGTGTACCAAGAACCAAGGTGAGTGTGCTGGTCAAGGCTTCTATCCAGCGACA	1204
QY	1121	TCGCGGTGGAGTGGGAGCAATGGGACCGCGGAGAAACAATACAAAGACCAACGCTCCCG	1180
DB	1205	TCGCGGTGGAGTGGGAGCAATGGGACCGCGGAGAAACAATACAAAGACCAACGCTCCCG	1264
QY	1181	TCGCTGGACTCCGACGGGCTCTTCTCTCTACAGCAAGCTCACCGTGGACAGCAGGT	1240

```

Db      1265 TGGTGTGACTCGAGCGCTCCTTTCTTCCTACAGCAAGCTCACCGTGGACAAGCAGGT 1324
Qy      1241 GGCAGCAGGGGAACGCTTCTTCTCATCTCCGTGATGCATGAGGCTCTTCACAACCACCTACA 1300
Db      1325 GCACAGAGGGGAACGCTTCTTCTCATCTCCGTGATGCATGAGGCTCTTCACAACCACCTACA 1384
Qy      1301 CGCAGAAGAGCCCTGCCCTGTCTCCGGGTAATGA 1335
Db      1385 CGCAGAAGAGCCCTGCCCTGTCTCCGGGTAATGA 1419

RESULT 10
US-09-822-830A-571
; Sequence 571, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 571
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-571

```



```
Db 537 TCTGGGGCACAGCGCCCTGGCTGCTCAAGGACTACTTCCCGAACCAGGTCAGC 596
QY 457 GGTCTGTGAAGTCAAGGCGCTGACAGCGCGTGCACACTTCCCGGCTGTCTACAG 516
Db 597 GTGTGTGAAGTCAAGGCGCTGACAGCGCGTGCACACTTCCCGGCTGTCTACAG 656
QY 517 TCTTCAGGACTTACTTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACC 576
Db 657 TCTTCAGGACTTACTTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGGCACC 716
QY 577 CAGACTTACATCTGAAGTGAATCACAAGCCAGCAACACCAAGGTCGACAAAGTG 636
Db 717 CAGACTTACATCTGAAGTGAATCACAAGCCAGCAACACCAAGGTCGACAAAGT 776
QY 637 GAGCCCAATCTGTGACAAACTCACACATGCCACCGTCCCGCAGCACTGAAGTCGG 696
Db 777 GAGCCCAATCTGTGACAAACTCACACATGCCACCGTCCCGCAGCACTGAAGTCCT 836
QY 697 GGGGACCGTCAGTCTTCTTCCCTCCCAAAACCCAGGACACCCCTCATGATCTCCGG 756
Db 837 GGGGACCGTCAGTCTTCTTCCCTCCCAAAACCCAGGACACCCCTCATGATCTCCGG 896
QY 757 ACCCTGAGTGCACATGCGTGTGTGACGTGAGCCAGCAAGACCCCTGAGGTCAAGTTC 816
Db 897 ACCCTGAGTGCACATGCGTGTGTGACGTGAGCCAGCAAGACCCCTGAGGTCAAGTTC 956
QY 817 AACTGGTACGTGGAGCGGTGAGTGCATATGCAAGACAAACCGCGGAGGAGCAG 876
Db 957 AACTGGTACGTGGAGCGGTGAGTGCATATGCAAGACAAACCGCGGAGGAGCAG 1016
QY 877 TACAACAGCAGTACCGTGTGTGAGCGTCTCACCGTCTGACAGGACTGCTGAAT 936
Db 1017 TACAACAGCAGTACCGTGTGTGAGCGTCTCACCGTCTGACAGGACTGCTGAAT 1076
QY 937 GCGAGGAGTACAAGTCAAGTCTCAACAAAGCCCTCCAGCCCTCCAGCCCTGCAAGAAC 996
Db 1077 GCGAGGAGTACAAGTCAAGTCTCAACAAAGCCCTCCAGCCCTCCAGCCCTGCAAGAAC 1136
QY 997 ATCTCCAAGCCAAAGGCGAGCCCGAGAACCCAGAGTGTACACCCCTGCCCCATCCCG 1056
Db 1137 ATCTCCAAGCCAAAGGCGAGCCCGAGAACCCAGAGTGTACACCCCTGCCCCATCCCG 1196
QY 1057 GATGAGTGCACAGAACCGTGTGAGCGTGTGACCTGCTGTGTCGTCGTCGTCGTCGTC 1116
Db 1197 GAGGAGTGCACAGAACCGTGTGAGCGTGTGACCTGCTGTGTCGTCGTCGTCGTCGTC 1256
QY 1117 GACATCGCGTGGAGTGGAGCAATGGCGAGCGCGGAGACACTACAAGACCCGCT 1176
Db 1257 GACATCGCGTGGAGTGGAGCAATGGCGAGCGCGGAGACACTACAAGACCCGCT 1316
QY 1177 CCGTGTGTGACTCCGAGCGCTCTTCTTCTTACAGCAAGCTCACCGTGGCAAGAGC 1236
Db 1317 CCGTGTGTGACTCCGAGCGCTCTTCTTCTTATAGCAAGCTCACCGTGGCAAGAGC 1376
QY 1237 AGTGGGAGCAGGGAAGCTTCTCATGCTGCTGCTGATGATGAGGCTCTGCACAAACC 1296
Db 1377 AGTGGGAGCAGGGAAGCTTCTCATGCTGCTGCTGATGATGAGGCTCTGCACAAACC 1436
QY 1297 TACAGCAGAGAGCGCTCTCCCTGCTCTCCGGTAAATGA 1335
Db 1437 TACAGCAGAGAGCGCTCTCCCTGCTCTCCGGTAAATGA 1475
```

RESULT 11

```
US-09-736-371B-20
; Sequence 20, Application US/09736371B
; Patent No. US20020131968A1
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Frewin, Mark
; TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES
; FILE REFERENCE: Waldmann
```

```
; CURRENT APPLICATION NUMBER: US/09/736, 371B
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 9815909.8
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: PCT/GB99/02380
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 1347
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1347)
US-09-736-371B-20
```

```
Query Match 85.0%; Score 1135; DB 10; Length 1347;
Best Local Similarity 91.4%; Pred. No. 1.4e-307;
Matches 1236; Conservative 0; Mismatches 90; Indels 27; Gaps 2;
```

```
QY 1 GAGGTGACGCTGGTGGAGCTCTGGGAGGAGGTTGGTAAAGCCCGGGGGTCCCTTAGACTC 60
Db 1 GAGGTCCAACGTGGAGTCTGGGGCGGTTTAGTCAGCCTGGAGGGTCCCTGAGACTC 60
QY 61 TCCTGTGCAGCTAGCGGATTTCAGTGGCTACTTTCAGTGGCTACTGGATGTCCTGGTCCGCCAGGCT 120
Db 61 TCCTGTGCAGCTTTCAGTGGCTACTTTCAGTGGCTTTCCTAATGGCTGGGTCCGCCAGGCT 120
QY 121 CCAGGGAAGGGGCTCGAGTGGTGGTGAATTTAGATTGAATCTGATATTAATATGCAACA 180
Db 121 CCAGGGAAGGGTCTGGAGTGGTCTCAACCATTTAG-----TACTAGTGGTGGTAGAACT 174
QY 181 CATTATCGGAGTCTGTGAAGGGAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
Db 175 TACTATGAGACTCCGTGAGGCGCGATTACTATCTCCAGAGATAATAGCAAAATACC 234
QY 241 CTCTATCTGCAATGAACAGCCCTGAAACCGAGGACACAGCCGCTGATTACTGTACA--- 297
Db 235 CTATACCTGCAATGAATAGTCTGAGGCTGAGGACACAGCCGCTGATTACTGTGCAAAA 294
QY 298 -----GATTTCTATAGACTGGGGCAGGGAACACTAGTCAACCGTCTCC 339
Db 295 TTTCGCGAGTACAGTGGTGGCTTTGATTACTTGGGGCAAGGGACCCCTGTCACGTCCTC 354
QY 340 TCAGCCCTCCACCAAGCGCCCTGCGCTTCCCGCTGGCACCCCTCTCCCAAGAGCACCTCT 399
Db 355 TCAGCCCTCCACCAAGGGCCCTCGGCTTCCCGCTGGCACCCCTCTCCCAAGAGCACCTCT 414
QY 400 GGGGCGACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTG 459
Db 415 GGGGCGACAGCGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCGCAACCGGTGACGGTG 474
QY 460 TCGTGAAGTCAAGCGCCCTGACGAGCGGTGACACACCTTCCCGGCTGTCTACAGTCC 519
Db 475 TCGTGAAGTCAAGCGCCCTGACGAGCGGTGACACACCTTCCCGGCTGTCTACAGTCC 534
QY 520 TCAGGACTCTACTTCCCTCAGCAGCGGTGACCGTCCCTCCAGAGCTTGGGCAACCCAG 579
Db 535 TCAGGACTCTACTTCCCTCAGCAGCGGTGACCGTCCCTCCAGAGCTTGGGCAACCCAG 594
QY 580 ACCTACATCTGCAACGTAATCACAAGCCAGCAACACCAAGGTGACAAAGAGTGGAG 639
Db 595 ACCTACATCTGCAACGTAATCACAAGCCAGCAACACCAAGGTGACAAAGAGTGGAG 654
QY 640 CCCAAATCTGTGACAAAACACTCACACATGCCACCGTCCCGCAGCACTGAATCTCGGGGG 699
Db 655 CCCAAATCTGTGACAAAACACTCACACATGCCACCGTCCCGCAGCACTGAATCTCGGGGG 714
QY 700 GCACCGTCAAGTCTTCTCTTCCCGCAAAACCCAGGACACCCCTCATGATCTCCCGGACC 759
Db 715 GGACCGTCAAGTCTTCTCTTCCCGCAAAACCCAGGACACCCCTCATGATCTCCCGGACC 774
```


Db 1136 GCGACATGCCCTGGAGTGGGAGAGCAATGGCAGCCGAGAAACACTACAGACCAGC 1195
QY 1175 CTTCCCGTGTGACTCCGACGCTCTCTTCTTCTCTACAGCAAGCTACCGTGGACAAGA 1234
Db 1196 CTTCCCGTGTGACTCCGACGCTCTCTTCTTCTCTACAGCAAGCTACCGTGGACAAGA 1255
QY 1235 GCAGGTGGCAGCAGGGAAGCTCTCTCATGCTCCGTCATCATGAGGCTCTGCACRACC 1294
Db 1256 GCAGGTGGCAGCAGGGAAGCTCTCTCATGCTCCGTCATGATGAGGCTCTGCACRACC 1315
QY 1295 ACTACACGAGAAGAGCTCTCCCTGTCTCCGGGTAAATGA 1335
Db 1316 ACTACACGAGAAGAGCTCTCTCTTAAGTCGGGGAATAA 1356

RESULT 13

US-10-066-895-14

; Sequence 14, Application US/10066895

; Patent No. US20020141990A1

; GENERAL INFORMATION:

; APPLICANT: Deen, Keith C.

; Dillon, Susan B.

; Porter, Terence C.

; Sweet, Raymond A.

; TITLE OF INVENTION: Human Monoclonal Antibodies

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESS: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19046

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/066,895

; FILING DATE: 04-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/297,344

; FILING DATE: 1999-JUN-09

; APPLICATION NUMBER: 60/030,149

; FILING DATE: 01-NOV-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Geiger, Kathleen

; REGISTRATION NUMBER: 35,880

; REFERENCE/DOCKET NUMBER: P50504

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-5968

; TELEFAX: 610-270-5090

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6284 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

; US-10-066-895-14

Query Match 84.6%; Score 1128.8; DB 12; Length 6284;
Best Local Similarity 91.2%; Pred. No. 1.2e-305;
Matches 1231; Conservative 0; Mismatches 92; Indels 27; Gaps 2;

QY 7 CAGCTGTGTGAGTCTGGGAGGCTGGTAAAGCCCGGGGGTCCCTTAGACTCTCTGT 66
Db 1081 CTGCTCAGGAGTCTGGGGGAGGCTGTGTCAGGCTGGCGGTCCCTAAGACTCTCTGT 1140

QY 67 GCAGCTAGCGGATTCACTTTTCAGTGGCTACTGGATGTCCTGGGTCCGCCAGGCTCCAGGG 126
Db 1141 GCAGCCTCTTGGAAACACACCTCAGTGGCTATACCATGCTGGTCCGCCAGGCTCCAGGG 1200
QY 127 AAGGGCTCGAGTGGGTGCTGAAATTTAGATTGAAATCTCATATTTATGCAACACATTTAT 186
Db 1201 AAGGGCTCGAGTGGGTGCTCATCAAT- - - - -ACTGGAGGTAGCAACTTCATAAACTAC 1254
QY 187 GCGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGACTGTAT 246
Db 1255 TCAGACTCAGTGAAGGCCGATTTCACCATCTCCAGAGACAACGCCAAGAACTCAGTTAT 1314
QY 247 CTGCAATGAACAGCCTGAAACCGGAGGACACAGCGTGTATTACTGT- - - - - 294
Db 1315 CTGCAATGAACAGCCTGACAGCCGAGGACACGGCTGTCTATTATTGTGCGACGCCCTT 1374
QY 295 - - - - -ACAGATTTTCATAGACTGGGGCCAGGGAACACTAGTCAACCGTCTCTCAGCC 345
Db 1375 ATAGCACCGCCTACTTTTGACCACCTGGGGCCAGGGAACCTGTCTACCGTCTCTCAGCC 1434
QY 346 TCCACCAAGGGCCCATCGGTCTTCCCGCTGGGACCCCTCTCCAAAGAGCACTCTCGGGGC 405
Db 1435 TCCACCAAGGGCCCATCGGTCTTCCCGCTGGGACCCCTCTCCAAAGAGCACTCTCGGGGC 1494
QY 406 ACAGCGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCGAAACCGGTGACGGTGTCTGG 465
Db 1495 ACAGCGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCGAAACCGGTGACGGTGTCTGG 1554
QY 466 AACTCAGGCGCCTGACACGCGGTGCACACCTTCCCGGCTGTCTACAGCTCTCAGGA 525
Db 1555 AACTCAGGCGCCTGACACGCGGTGCACACCTTCCCGGCTGTCTACAGCTCTCAGGA 1614
QY 526 CTCTACTCTCCTCAGCAGCGTGGTGACCGTGGCCCTCAGCAGCTTGGGGACCCAGACCTAC 585
Db 1615 CTCTACTCTCCTCAGCAGCGTGGTGACTGTGCCCTCCAGCAGCTTGGGGACCCAGACCTAC 1674
QY 586 ATCTGCAAGCTGAATCACAAGCCCAAGCAACACCAAGGTGGACAAGAAAGTGAGGCCAAA 645
Db 1675 ATCTGCAAGCTGAATCACAAGCCCAAGCAACACCAAGGTGGACAAGAAAGTTAGGCCAAA 1734
QY 646 TCTTGTGACAAAAGTCAACATGCGCCACCGTGCAGCAGCTGAACTCGCGGGGACCG 705
Db 1735 TCTTGTGACAAAAGTCAACATGCGCCACCGTGCAGCAGCTGAACTCGCGGGGACCG 1794
QY 706 TCAGTCTTCTCTTCCCGCCCAAGCAACCAAGGACCCCTCATGATCTCCCGGACCCCTGAG 765
Db 1795 TCAGTCTTCTCTTCCCGCCCAAGCAACCAAGGACCCCTCATGATCTCCCGGACCCCTGAG 1854
QY 766 GTCACATGCTGTGTGGTGGACGTGAGCCACGAGACCCCTGAGGTCAAGTTCAACTGGTAC 825
Db 1855 GTCACATGCTGTGTGGTGGACGTGAGCCACGAGACCCCTGAGGTCAAGTTCAACTGGTAC 1914
QY 826 GTGGACGGCGTGGAGTGCATATGCCAGACAAGCCCGGGGAGGAGCAGTACACAGC 885
Db 1915 GTGGACGGCGTGGAGTGCATATGCCAGACAAGCCCGGGGAGGAGCAGTACACAGC 1974
QY 886 AGGTACCGTGTGTGCTCAGCGTCTCTCAGCGTCTGACCGAGCTGCTGAATGGCAAGGAG 945
Db 1975 AGGTACCGGCTGTGCTCAGCGTCTCTCAGCGTCTGACCGAGCTGCTGAATGGCAAGGAG 2034
QY 946 TACAAGTGAAGTCTTCCAAACAAAGCCCTCCAGCGCCCATCGAGAAAACCATCTCCAAA 1005
Db 2035 TACAAGTGAAGTCTTCCAAACAAAGCCCTCCAGCGCCCATCGAGAAAACCATCTCCAAA 2094
QY 1006 GCCAAGGCGCAGCCCGAGAACACAGGTGTACACCCCTGCCCGCATCCCGGATGAGCTG 1065
Db 2095 GCCAAGGCGCAGCCCGAGAACACAGGTGTACACCCCTGCCCGCATCCCGGATGAGCTG 2154
QY 1066 ACCAAGAACAGGTGAGCTGACCTGCCTGGTCAAGGCTTCTATCCAGGACATCCGCC 1125
Db 2155 ACCAAGAACAGGTGAGCTGACCTGCCTGGTCAAGGCTTCTATCCAGGACATCCGCC 2214
QY 1126 GTGGAGTGGGAGCAATGGGCGAGCCCGGAGAAACAACTACAAGAACACCGCTCCCGTGTG 1185

APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakara
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822.849A
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 103
LENGTH: 1598
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1040,1562
OTHER INFORMATION: n = a,c,t, or g
US-09-822-849A-103

Query Match 82.8%; Score 1105.2; DB 10; Length 1598;
Best Local Similarity 89.8%; Pred. No. 3.2e-299;
Matches 1220; Conservative 0; Mismatches 109; Indels 30; Gaps 2;
QY 1 GAGGTGACGTGGTGGAGTCTGGGGAGGCTTGTAAAGCCCGGGGGTCCCTTAGACTC 60
DB 120 GAGGCGCAGCTGTGACGTCTGGGGAGAAATGTGTGAGCTGGAGGTCGGTGGAGACTC 179
QY 61 TCCTGTGACGTAGCGGTTTACATTTTCAGTGGCTACTGGATGTCTTGGTGGCGGAGGCT 120
DB 180 TCCTGTGAGGCTCTGGATTCCTCCCTTAGAAATTCAGAAATGAATTTGGTCCGCGCAGGCT 239
QY 121 CCAGGGAAGGGCTCGAGTGGCTGAAATAGATTGAAATCTGATAATTTGCAACA 180
DB 240 CCAGGGAAGGGCTGGATTTATCATCATCAGTAGCA-----CTGGCAATTCGAAA 293
QY 181 CATTTATGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
DB 294 TATTACGACAGCTCTGTGAAGGGTCGCTTGCCTATCTCAAGGGACGAGTGTCTACTGTGGCAGA 353
QY 241 CTGTATCTGCAAAATGAACAGGCTGAAACCGAGGACACAGCCGTGTATTACTGTAC----- 296
DB 354 CTCTTCTACATTTGACAGGCTGAGACCCGAGACAGGCTGTCTACTGTGTGGCAGA 413
QY 297 -----AGATTTCATAGACTGGGGCCAGGGACACACTAGTCACCGTC 336
DB 414 GACCTGAGAGTAGTGAACGGAGGCTTCGACCCGTGGGGCCAGGAGGCTGGTCCCTCGTC 473
QY 337 TCCTCAGGCTCCAGCAGGGCCCATCGGTCTTCCCTCGGACCCCTCTCCCAAGAGACC 396
DB 474 TCCTCAGGCTCCAGCAGGGCCCATCGGTCTTCCCTCGGACCCCTCTCCCAAGAGACC 533
QY 397 TCTGGGGCAGCAGGGCCCTGGGTGCTGTCAAGGACTACTTCCCGGAACCGGTGACG 456
DB 534 TCTGGGGCAGCAGGGCCCTGGGTGCTGTCAAGGACTACTTCCCGGAACCGGTGACG 593
QY 457 GTGTCTGGAACTCAGCGGCCCTGACACAGGGCTGTGCACACCTTCCCGGTGTCTACAG 516
DB 594 GTGTCTGGAACTCAGCGGCCCTGACACAGGGCTGTGCACACCTTCCCGGTGTCTACAG 653
QY 517 TCCTCAGGACTCTACTCCCTCAGCAGGCTGTGACCGTGTGACCGTGTGACCGTGTGGGACC 576
DB 654 TCCTCAGGACTCTACTCCCTCAGCAGGCTGTGACCGTGTGACCGTGTGACCGTGTGGGACC 713
QY 577 CAGACCTACATCTGCAACGTGAATCAAGCCCGAGCAACACCAAGGTGGACAGAAAGTG 636
DB 714 CAGACCTACATCTGCAACGTGAATCAAGCCCGAGCAACCAAGGTGGACAGAAAGTG 773
QY 637 GAGCCCAAAATCTTTGTGACAAAACCTACACATGCCCGGTGCCAGCACTGAACCTCGG 696
DB 774 GAGCCCAAAATCTTTGTGACAAAACCTACACATGCCCGGTGCCAGCACTGAACCTCTG 833

QY 697 GGGGACCCGTGAGTCTTCTCTTCCCGCCAAAACCCCAAGGACACCCCTCATGTCTCCCG 756
DB 834 GGGGACCCGTGAGTCTTCTCTTCCCGCCAAAACCCCAAGGACACCCCTCATGTCTCCCG 893
QY 757 ACCCTGAGGTACATCGGTGGTGGAGGTGAGCCACGAAGACCCCTGAGGTCAAGTTC 816
DB 894 ACCCTGAGGTACATCGGTGGTGGAGGTGAGCCACGAAGACCCCTGAGGTCAAGTTC 953
QY 817 AACTGTGTGAGTGGAGCGGTGGAGTGTGATAATGCCAAGAACGCGGGAGGAGCAG 876
DB 954 AACTGTGTGAGTGGAGCGGTGGAGTGTGATAATGCCAAGAACGCGGGAGGAGCAG 1013
QY 877 TACAACAGCACGTACCGTGTGGTTCAGGTCTCTCAGCGTCTGACACAGGACTGGTGAAT 936
DB 1014 TACAACAGCACGTACCGTGTGGTTCAGGTCTCTCAGCGTCTGACACAGGACTGGTGAAT 1073
QY 937 GGCAAGGAGTACAAGTGCAAGGTCTCCAAAGAGCCCTCCAGCCCGCCCATCGAGAAACC 996
DB 1074 GGCAAGGAGTACAAGTGCAAGGTCTCCAAAGAGCCCTCCAGCCCGCCCATCGAGAAACC 1133
QY 997 ATCTCAAAGCCAAAGGGAGCGCCCGAGAACACACAGGTGTACACCTGCCCGCCATCCCGG 1056
DB 1134 ATCTCAAAGCCAAAGGGAGCGCCCGAGAACACACAGGTGTACACCTGCCCGCCATCCCGG 1193
QY 1057 GATGAGCTGACCAAGAACACAGGTTCAGCTGCTGCTGCTCAAGGCTTCTATCCAGC 1116
DB 1194 GAGGAGTACCAAGAACACAGGTTCAGCTGCTGCTGCTCAAGGCTTCTATCCAGC 1253
QY 1117 GACATCGCGTGGAGTGGAGAGCAATGGCAGCGCCGAGAACAACTACAGACCCAGCCT 1176
DB 1254 GACATCGCGTGGAGTGGAGAGCAATGGCAGCGCCGAGAACAACTACAGACCCAGCCT 1313
QY 1177 CCGTGTGAGTCCGACCGCTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCAC 1236
DB 1314 CCGTGTGAGTCCGACCGCTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCAC 1296
QY 1237 AGTGGCAGCAGGGGAACTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCAC 1373
DB 1374 AGTGGCAGCAGGGGAACTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCAC 1433
QY 1297 TACACGCAAGAGGCTCTCCCTGTCTCCGGGTAAATGA 1335
DB 1434 TACACGCAAGAGGCTCTCCCTGTCTCCGGGTAAATGA 1472

Search completed: April 26, 2003, 09:24:37

Job time : 153.024 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 26, 2003, 04:57:16 ; Search time 55.2959 Seconds
(without alignments)
7404.053 Million cell updates/sec

Title: US-09-674-716B-18

Perfect score: 1335
Sequence: 1 gaggtgcagctggtgagtc.....ccctgtctccgggtaaatga 1335

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.*

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1147.2	85.9	1437	3	US-08-487-550-7
2	1143.6	85.7	1576	1	US-08-157-101A-6
3	1141.2	85.5	19040	4	US-09-343-485A-3
4	1140.6	85.4	1350	1	US-08-157-101A-9
5	1082.6	81.1	8120	3	US-09-027-449-68
6	1082.6	81.1	8120	3	US-09-026-985-68
7	1082.6	81.1	8120	4	US-09-121-952A-68
8	1082.6	81.1	8120	4	US-09-234-340A-68
9	1066.4	79.9	1655	3	US-09-049-672A-21
10	1063.4	79.7	6557	1	US-08-286-740-3
11	1063.4	79.7	6557	5	PCT-US93-09576-3
12	1042.6	78.1	1617	2	US-08-378-939-9
13	1040.6	77.9	1431	3	US-08-487-550-11
14	1039.8	77.9	1418	4	US-08-793-450-7
15	1039.8	77.9	9209	1	US-08-149-099C-3
16	1039.8	77.9	9209	1	US-08-476-275-2
17	1039.8	77.9	9209	2	US-08-478-567A-3
18	1039.8	77.9	9209	4	US-08-475-815B-3
19	1039.8	77.9	18986	2	US-08-819-866-2
20	1039.8	77.9	18986	2	US-09-023-715-2
21	1039.8	77.9	18986	4	US-09-343-485A-2
22	1039	77.8	1567	3	US-09-049-672A-17
23	1035	77.5	1329	5	PCT-US96-13152-3
24	1021.4	76.5	1431	3	US-08-487-550-3
25	1020.6	76.4	1404	4	US-09-485-737B-66
26	1020.6	76.4	2133	4	US-09-485-737B-89
27	1018.6	76.3	1428	1	US-08-488-376-19

Query Match

85.9%; Score 1147.2; DB 3; Length 1437;

ALIGNMENTS

RESULT 1
US-08-487-550-7

; Sequence 7, Application US/08487550

; Patent No. 6113898

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,550

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1437 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1437

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: 1..1437

; US-08-487-550-7

Query Match	85.7%	Score 1143.6;	DB 1;	Length 1576;
Best Local Similarity	91.6%;	Pred. No. 4.6e-263;		
Matches 1244;	Conservative	0; Mismatches	84;	Indels 30; Gaps 2

QY	2	AGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGTGAAGCCGGGGGGTCCCTTGAGACTCT	61
DB	43	AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGGTGCCAGCTGGGAGGTCCCTTGAGACTCT	102
QY	62	CCTGTGCAGCTAGCGGATTCACCTTCAGTGGCTACTGGATGTCTGGGTCCGCCAGGCTC	121
DB	103	CCTGTGCAGCTCTGGATTCACCTTCAGTAGCAATTTCTATGCACTGGGTCCGCCAGGCTC	162
QY	122	CAGGGAAGGGCTCGAGTGGGTTGCTGAAATTAGATTGAANTCTGATAATTATGCAACAC	181
DB	163	CAGCAAGGGGTTGGAGTGGGTGGCAGTTA-----TATTATATGATGAATCATATAAT	216
QY	182	ATTATGCGGAGTCTGCAAGGGGAATTCACCATCTCAAGAGATGATTCAAATCTAGAC	241
DB	217	TCTAGCAGACTCGTGAAGGGCGGATTACCAATTTCCAGAGACAAATCCAAGAACACAC	276
QY	242	TGTATCTGCAANTGAACAGACTGAAACCGAGAGACACAGCCGTGTATTACTGTACA----	297
DB	277	TGTATCTGGAAGTGAAGAGCCTGCAAACTGAGGACACGGGTGTCTATTACTCTATAAGN	336
QY	298	-----GATTTCATAGACTGGGGCCAGGGAACACTAGTTCACCGTCT	337
DB	337	ATCAAACTTACGGAGTCCACAGATTTGACTCTCGGGCCAGGGAACCTGTGTACCGTCT	396
QY	338	CCTCAGCCTCCACAAGGGCCCATCGGTCTTCCCTCGCACCCCTCTCCAAGAGCACT	397
DB	397	CCTCAGCCTCCACAAGGGCCCATCGGTCTTCCCTCGCACCCCTCTCCAAGAGCACT	456
QY	398	CTGGGGCACAGGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGAACCCTGTGACGG	457
DB	457	CTGGGGCACAGGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGAACCCTGTGACGG	516
QY	458	TGTCGTGAACTCAGGCGCCCTCACAGCGGGTGACACCTTCGGGTGTCTCTACAGT	517
DB	517	TGTCGTGAACTCAGGCGCCCTGGCCAGCGGGTGGACACCTTCCCGGTGTCTCTACAGT	576
QY	518	CCTCAGGACTCTACTCCCTCAGCAGCGGTGGTGACCGTGCCTTCCAGCAGCTTGGCAACC	577
DB	577	CCTCAGGACTCTACTCCCTCAGCAGCGGTGGTGACCGTGCCTTCCAGCAGCTTGGCAACC	636
QY	578	AGACCTACATCTCAACGTTGAATCAACGCCAGCAACCAACCAAGGTGGACAAAGAATGG	637
DB	637	AGACCTACATCTCAACGTTGAATCAACGCCAGCAACCAACCAAGGTGGACAAAGAATGG	696
QY	638	AGCCCAATCTGTGCAAAACTCACATGCCACCGTGCCTTCCAGCAGCTGAACCTCGCGG	697
DB	697	AGCCCAATCTGTGCAAAACTCACATGCCACCGTGCCTTCCAGCAGCTGAACCTCGCGG	756
QY	698	GGGACCGTCACTTTCCTTCCCCCAAAACCCCAAGGACACCTCATGTCTCCCGGA	757
DB	757	GGGACCGTCACTTTCCTTCCCCCAAAACCCCAAGGACACCTCATGTCTCCCGGA	816
QY	758	CCCTCAGGTCACATCGTGGTGGAGCTGAGCCAGGAAGACCTCGAGGTCAAGTTCA	817
DB	817	CCCTCAGGTCACATCGTGGTGGAGCTGAGCCAGGAAGACCTCGAGGTCAAGTTCA	876
QY	818	ACTGGTACGTGGACGGCTGGAGTGCATAATGCCAAGCAAAAGCCCGGAGGAGCAGT	877
DB	877	ACTGGTACGTGGACGGCTGGAGGTGCATAATGCCAAGCAAAAGCCCGGAGGAGCAGT	936
QY	878	ACAACGACGTACCGCTGGTGGTCAGCGTCTCACCGTCTGCACGAGCAGTGGCTGAATG	937
DB	937	ACAACGACGTACCGGGTGGTCAGCGTCTCACCGTCTGCACGAGCAGTGGCTGAATG	996
QY	938	GCAAGAGTACAAGTCAAGGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAAAACA	997
DB	997	GCAAGAGTACAAGTCAAGGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAAAACA	1056
QY	998	TCTCCAAAGCAAAAGGACCGCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGG	1057
DB	1057	TCTCCAAAGCAAAAGGACCGCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGG	1116
QY	1058	ATGAGTGTACCAAGAACACAGGTGACCTGGCTGCTGCTCAAGGCTTCTATCCCAAGCG	1117

Db	1117	ATGAGCTGACAGAGACCGAGT	CAGCCTGACCTGCTGCTCAAGAGCTT	CTATCCAGCG	1176
Qy	1118	ACATCGCGTGGAGTGGGAGAGCAAT	GGGACGCCGGAGAACCACT	TACAAGACCAACGCCTC	1177
Db	1177	ACATCGCGTGGAGTGGGAGAGCAAT	GGGACGCCGGAGAACCACT	TACAAGACCAACGCCTC	1236
Qy	1178	CCGTGCTGGAGACTCCGACGGCTCT	TCTCTTCTACAGCAAGCTCACCGT	TGACACAGAGCA	1237
Db	1237	CCGTGCTGGAGACTCCGACGGCTCT	TCTCTTCTACAGCAAGCTCACCGT	TGACACAGAGCA	1296
Qy	1238	GGTGGCAGCAGGGAGCGCTTCTCAT	GCTCCGTGATGATGAGGCTCTGC	CACACCACT	1297
Db	1297	GGTGGCAGCAGGGAGCGCTTCTCAT	GCTCCGTGATGATGAGGCTCTGC	CACACCACT	1356
Qy	1298	ACAGCAGAGAGCCCTCTCCCTGTC	TCCGGGTAAATGA	1335	
Db	1357	ACAGCAGAGAGCCCTCTCCCTGTC	TCCGGGTAAATGA	1394	

RESULT 3

```

US-09-343-485A-3
; Sequence 3, Application US/09343485A
; Patent No. 641377
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL R.
; APPLICANT: BARNETT, RICHARD S.
; APPLICANT: MCLACHLAN, KAREN R.
; TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN
; TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND
; TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
; FILE REFERENCE: 037003-0275807
; CURRENT APPLICATION NUMBER: US/09/343,485A
; CURRENT FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/023,715
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 08/819,866
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 19040
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: referred to as "Mandy"
US-09-343-485A-3

```

Query Match 85.5%; Score 1141.2; DB 4; Length 19040;
Best Local Similarity 92.0%; Pred. No. 3.6e-262;
Matches 1246; Conservative 0; Mismatches 83; Indels† 25; Gaps 3;

Query Match 85.5%; Score 1141.2; DB 4; Length 19040;
Best Local Similarity 92.0%; pred. No. 3.6e-262;
Matches 1246; Conservative 0; Mismatches 83; Indels 25; Gaps


```
QY 338: CCTCAGCCTCCACCAAGGCCCATCGGCTTCCCCCTGGCACCCCTCTCCCAAGAGCACCT 397
Db 356: CCTCAGCCTCCACCAAGGCCCATCGGCTTCCCCCTGGCACCCCTCTCCCAAGAGCACCT 415
QY 398: CTGGGGGACACAGCGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCGAAACCGGTGAGGG 457
Db 416: CTGGGGGACACAGCGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCGAAACCGGTGAGGG 475
QY 458: TGTCGTGGAACTCAGCGCCCTGACACAGCGGGGTGCACACCTTCCCGGCTCTCTACAGT 517
Db 476: TGTCGTGGAACTCAGCGCCCTGACACAGCGGGGTGCACACCTTCCCGGCTCTCTACAGT 535
QY 518: COTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCC 577
Db 536: COTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGCACCC 595
QY 578: AGACCTACATCTGCAACGTGAATCAAGCCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 637
Db 596: AGACCTACATCTGCAACGTGAATCAAGCCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 655
QY 638: AGCCCAAACTTGTGACAAAATCACAATGCCACCGTGCACCGTCCAGCAGCTGAACCTCGGG 697
Db 656: AGCCCAAACTTGTGACAAAATCACAATGCCACCGTGCACCGTCCAGCAGCTGAACCTCGGG 715
QY 698: GGGCACCCTGAGTCTCTCTTCCCCCAAAACCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 757
Db 716: GGGCACCCTGAGTCTCTCTTCCCCCAAAACCAAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 775
QY 758: CCCCTGAGGTACATCGTGGTGGTGGAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTCA 817
Db 776: CCCCTGAGGTACATCGTGGTGGTGGAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGTCA 835
QY 818: ACTGTGACTGGACGGCTGGAGTGCATAATGCCAGACAAAGCCGCGGAGGAGCAGT 877
Db 836: ACTGTGACTGGACGGCTGGAGTGCATAATGCCAGACAAAGCCGCGGAGGAGCAGT 895
QY 878: ACAACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 937
Db 896: ACAACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 955
QY 938: GCAAGGAGTACAGTGCAGGCTCTCCACAAAGCCCTCCAGCAGCAGCAGCAGCAGCAGCAGC 997
Db 956: GCAAGGAGTACAGTGCAGGCTCTCCACAAAGCCCTCCAGCAGCAGCAGCAGCAGCAGCAGC 1015
QY 998: TCTCCAAAGCCAAAGGCGAGCCGAGAACCCACAGGTGTACACCGTGCACCGCTCCCGCCATCCCGGG 1057
Db 1016: TCTCCAAAGCCAAAGGCGAGCCGAGAACCCACAGGTGTACACCGTGCACCGCTCCCGCCATCCCGGG 1075
QY 1058: ATGAGCTGACCAAGAACAGGTGACGCTGACCTGCCCTGGTCAAGAGGCTTCTATCCCGAGCG 1117
Db 1076: ATGAGCTGACCAAGAACAGGTGACGCTGACCTGCCCTGGTCAAGAGGCTTCTATCCCGAGCG 1135
QY 1118: ACATCGCGTGGAGTGGGAGAGCAATGGCAGCCGAGAGACAACTACAAGACCAAGAGCA 1177
Db 1136: ACATCGCGTGGAGTGGGAGAGCAATGGCAGCCGAGAGACAACTACAAGACCAAGAGCA 1195
QY 1178: CCGTCTGGACTCCGAGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAAAGAGCA 1237
Db 1196: CCGTCTGGACTCCGAGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAAAGAGCA 1255
QY 1238: GGTGGCAGCGGGAAGCTCTTCTATGTCGCTGATGATGAGGCTCTGCACAAACACT 1297
Db 1256: GGTGGCAGCGGGAAGCTCTTCTATGTCGCTGATGATGAGGCTCTGCACAAACACT 1315
QY 1298: ACAGCAGAGAGGCTCTCCCTGTCTCCGGGTAAA 1332
Db 1316: ACAGCAGAGAGGCTCTCCCTGTCTCCGGGTAAA 1350
```

RESULT 5

US-09-027-449-68

; Sequence 68, Application US/09027449

```
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8120 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-09-027-449-68
```

```
Query Match 81.1%; Score 1082.6; DB 3; Length 8120;
Best Local Similarity 88.6%; Pred. No. 2.4e-248;
Matches 1210; Conservative 0; Mismatches 119; Indels 36; Gaps 2;
```

```
QY 1 GAGGTGCAGTGGTGGAGTCTGGGGAGGCTGGTAAAGCCGGGGGTCCCTTAGACTC 60
Db 1363 GAAGTTACAGTAGTCAGTCTGGCGTGGCTGGTGACCCAGGGGGCTCACTCGGTTG 1422
QY 61 TCCTGTGACGTAGCGGATTCACCTTTCAGTGGCTACTGGATGTCTCTGGGTCCGCCAGGCT 120
Db 1423 TCCTGTGACGTCTGGCTACTCTCTTCGAGTCACTATATGACATGGTGGTCCGTCAGGCC 1482
QY 121 CCAGGGAAGGGGTCAGTGGGTGGTGGTGAATAGATTCGAATCTGATTAATATGCAACA 180
Db 1483 CCGGGTAAGGGGCTGGAATGGGTGGATATATTT-----GATCCTTCCAATGGTGAACCT 1536
QY 181 CATTATCGGAGTCTCTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
Db 1537 ACGTATAATCAAAAGTTCAAGGGCGCTTTCACCTTATCTCGCGACACTCCAAAACACA 1596
QY 241 CTGTATCTGCAATGAACACCGCTGAAACCGAGGACACAGCGCTGTATTAATCTGTACA--- 297
Db 1597 GCATACCTGCAGATGAACACCGCTGCGTGTGAGGACACTGGCGCTCTATTACTGTGCAAGA 1656
QY 298 -----GATTTTCATAGACTGGGGCCAGGGACACTAGTC 330
Db 1657 GGGGATTATCGCTACAATGGTGAATGGTTCCTTCGAGCTCGGGGTCAAGGAACCCCTGTC 1716
```

```
Qy 331 ACCGTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGACACCTCTCTCAAG 390
Db 1717 ACCGTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGACACCTCTCTCAAG 1776
Qy 391 AGCACCCTCTGGGGGCACAGGGCCCTGGGTCTGCTGCTGAAGACTACTTCCCGCAACCG 450
Db 1777 AGCACCCTCTGGGGGCACAGGGCCCTGGGTCTGCTGCTGAAGACTACTTCCCGCAACCG 1836
Qy 451 GTGACGGTGTCTGGAACCTCAGGGCCCTGACCAAGCGGCTGCACACCTTCCCGGGTGTG 510
Db 1837 GTGACGGTGTCTGGAACCTCAGGGCCCTGACCAAGCGGCTGCACACCTTCCCGGGTGTG 1896
Qy 511 CTACAGTCTCAGAGCTCTACTTCCCTCAGCAGCGTGTGACCGGTGCGCCTCCAGCAGCTTG 570
Db 1897 CTACAGTCTCAGAGCTCTACTTCCCTCAGCAGCGTGTGACCGGTGCGCCTCTAGCAGCTTG 1956
Qy 571 GGCACCCAGACCTACATCTGCAAGCTGAATCACAAGCCCGCAGCACACCAAGGTGGACAAG 630
Db 1957 GGCACCCAGACCTACATCTGCAAGCTGAATCACAAGCCCGCAGCACACCAAGGTGGACAAG 2016
Qy 631 AAAGTGGAGCCCAATCTTGTGACAAACTCACACATGCCACCGTCCCGCAGCACCTGAA 690
Db 2017 AAAGTGGAGCCCAATCTTGTGACAAACTCACACATGCCACCGTCCCGCAGCACCTGAA 2076
Qy 691 CTCGGGGGGCACCCTGAGTCTTCTTCTCCCGCCAAACCCCAAGAGACACCTCATGATC 750
Db 2077 CTCGGGGGGCACCCTGAGTCTTCTTCTCCCGCCAAACCCCAAGAGACACCTCATGATC 2136
Qy 751 TCCGGGACCCCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 810
Db 2137 TCCGGGACCCCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 2196
Qy 811 AAGTTCACCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 870
Db 2197 AAGTTCACCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 2256
Qy 871 GAGCAGTACACAGCAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 930
Db 2257 GAGCAGTACACAGCAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2316
Qy 931 CTGAATGCAAGGAGTACAAAGTCAAGTCTTCCAAAGCCCTCCAGCCCTCCAGCCCTCCAG 990
Db 2317 CTGAATGCAAGGAGTACAAAGTCAAGTCTTCCAAAGCCCTCCAGCCCTCCAGCCCTCCAG 2376
Qy 991 AAAACCATCTCCAAAGCCAAAGGAGCCCGGAGAACACAGAGTGTACACCTGCCCCCA 1050
Db 2377 AAAACCATCTCCAAAGCCAAAGGAGCCCGGAGAACACAGAGTGTACACCTGCCCCCA 2436
Qy 1051 TCCCGGGATGAGCTACCAAGAACCCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 1110
Db 2437 TCCCGGGATGAGCTACCAAGAACCCAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 2496
Qy 1111 CCCAGCAGATCGCGTGGAGTGGAGAGCAATGGGAGCCCGGAGAACCACTACAAGACC 1170
Db 2497 CCCAGCAGATCGCGTGGAGTGGAGAGCAATGGGAGCCCGGAGAACCACTACAAGACC 2556
Qy 1171 AGCGCTCCCGTGGAGTCCGAGCGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1230
Db 2557 AGCGCTCCCGTGGAGTCCGAGCGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2616
Qy 1231 AAGCAGGTGGCAGCAGGGGAAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1290
Db 2617 AAGCAGGTGGCAGCAGGGGAAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2676
Qy 1291 AACCACTACAGCAGAGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1335
Db 2677 AACCACTACAGCAGAGAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2721
```

```
; GENERAL INFORMATION:  
; APPLICANT: Gonzalez, Tania R.  
; APPLICANT: Leong, Steven R.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
; Humanized Anti-IL-8 Monoclonal Antibodies  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/026,985  
; FILING DATE: 20-Feb-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P1085R3-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-5530  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 68:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8120 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; US-09-026-985-68  
  
Query Match 81.1%; Score 1082.6; DB 3; Length 8120;  
Best Local Similarity 88.6%; Pred. No. 2.4e-248;  
Matches 1210; Conservative 0; Mismatches 119; Indels 36; Gaps 2;  
  
Qy 1 GAGGTGACGTGGTGGAGTCTGGGGAGGCTGGTAAAGCCCGGGGGTCCCTTAGACTC 60  
Db 1363 GAAGTTCAGCTAGTCGAGTCTGGCGGTGGCTGGTGCACGAGGGGCTCACTCCGTTG 1422  
Qy 61 TCCTGTGACGTAGCGGATTCACCTTTCAGTGGCTACTGGATGCTCCTGGGTCCGCGAGGCT 120  
Db 1423 TCCTGTGACGTCTGGCTACTCCTTTCGAGTCACTATATGCACTGGGTCCGTCAGGCC 1482  
Qy 121 CAGGGAAGGGCTCGAGTGGGTGCTGAAATAGATTTGAAATCTGATAATTAATGCAACA 180  
Db 1483 CCGGGTAAGGGCTCGAAATGGGTGGATATAT-----GATCCTTCCAAATGGTGAAC 1536  
Qy 181 CATTATGCGGAGTCTGGAAGGGGAAATTCACATCTCAAGAGATGATTCAAAATCTAGA 240  
Db 1537 ACGTATAATCAAAAGTTCAAGGGCCCTTTCACCTTATCTCGGACAACTCCAAACACA 1596  
Qy 241 CTGTATCTCAAAATGAACAGCCCTGAAAACCGAGGACACAGCCGTGTATTACTGTACA--- 297  
Db 1597 GCATACCTGCAGATGAACAGCCCTGCGTGTGAGGACACTGCGGTCTATTACTGTGCAAGA 1656  
Qy 298 -----GATTTCAATAGCTGGGGCCGAGGAACACTAGTC 330  
Db 1657 GGGGATTATCGCTACAAATGGTACTGGTCTTCGAGCTTGGGGTCAAGGAACCTGGTTC 1716  
Qy 331 ACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGACACCTCTCTCCAAAG 390  
Db 1717 ACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGACACCTCTCTCCAAAG 1776  
Qy 391 AGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGACTACTTCCCGCAACCG 450  
Db 1777 AGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGACTACTTCCCGCAACCG 1836
```

```
QY 451 GTGACGGTGTCTGTGAAGTCTAGGCGCCTGACAGCGCGTGCACACCTTCCCGGCTGTC 510
Db 1837 GTGACGGTGTCTGTGAAGTCTAGGCGCCTGACAGCGCGTGCACACCTTCCCGGCTGTC 1896
QY 511 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTG 570
Db 1897 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTG 1956
QY 571 GGCACCCAGACCTACATCTGAAGTGAATCAGAGCCAGCAGCAGCAGCAGGTTGGACAAG 630
Db 1957 GGCACCCAGACCTACATCTGAAGTGAATCAGAGCCAGCAGCAGCAGCAGGTTGGACAAG 2016
QY 631 AAGTGGAGCCCAACTTGTGACAAACTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 690
Db 2017 AAGTGGAGCCCAACTTGTGACAAACTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2076
QY 691 CTCGGGGGACCGTCACTCTTCTCTTCCCCCAAAACCCAGCAGCAGCAGCAGCAGCAGCAG 750
Db 2077 CTCGGGGGACCGTCACTCTTCTCTTCCCCCAAAACCCAGCAGCAGCAGCAGCAGCAGCAG 2136
QY 751 TCCGGGACCCCTGAGGTACATCTGCTGTGACGTGAGCCAGCAGCAGCAGCAGCAGCAGCAG 810
Db 2137 TCCGGGACCCCTGAGGTACATCTGCTGTGACGTGAGCCAGCAGCAGCAGCAGCAGCAGCAG 2196
QY 811 AAGTTCAACTGTTAGTGGAGCGGTGGAGTGCATATGCCAAGACAAAGCCGCGGGAG 870
Db 2197 AAGTTCAACTGTTAGTGGAGCGGTGGAGTGCATATGCCAAGACAAAGCCGCGGGAG 2256
QY 871 GAGCAGTACACACGACGTACCGTGTGTCAGCTCTCAGCGTCTGTCAGCAGCAGCAGCAGCAG 930
Db 2257 GAGCAGTACACACGACGTACCGTGTGTCAGCTCTCAGCGTCTGTCAGCAGCAGCAGCAGCAG 2316
QY 931 CTGAATGCGAGGAGTACAAAGTCAAGTGTCTCCAAAGAGCCCTCCAGCAGCAGCAGCAGCAG 990
Db 2317 CTGAATGCGAGGAGTACAAAGTCAAGTGTCTCCAAAGAGCCCTCCAGCAGCAGCAGCAGCAG 2376
QY 991 AAACCATCTCCAAGCAAGGCGCAGCCGCGGAGCAATGGGAGCAATGGGAGCAATGGGAGCA 1050
Db 2377 AAACCATCTCCAAGCAAGGCGCAGCCGCGGAGCAATGGGAGCAATGGGAGCAATGGGAGCA 2436
QY 1051 TCCGGGATGAGTGCACCAAGACAGGTGAGTGTGACGTGACCTGCTGCTGCTGCTGCTGCTGCT 1110
Db 2437 TCCGGGATGAGTGCACCAAGACAGGTGAGTGTGACGTGACCTGCTGCTGCTGCTGCTGCTGCT 2496
QY 1111 CCCAGCAGATCGCCGTGGAGTGGAGAGCAATGGGAGCAATGGGAGCAATGGGAGCAATGGGAG 1170
Db 2497 CCCAGCAGATCGCCGTGGAGTGGAGAGCAATGGGAGCAATGGGAGCAATGGGAGCAATGGGAG 2556
QY 1171 ACGCTCCCGTGTGGAGTCCGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1230
Db 2557 ACGCTCCCGTGTGGAGTCCGAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2616
QY 1231 AAGAGAGGTGGCAGCAGGGAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1290
Db 2617 AAGAGAGGTGGCAGCAGGGAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2676
QY 1291 AACCACTACAGCAGAGAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1335
Db 2677 AACCACTACAGCAGAGAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2721
```

RESULT 7

```
US-09-121-952A-68
: Sequence 68, Application US/09121952A
: Patent No. 6458355
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc., Hsei, Vanessa
: APPLICANT: Koumenis, Iphigenia
: APPLICANT: Leong, Steven R.
: APPLICANT: Presta, Leonard G.
: APPLICANT: Shirokhi, Zahra
: APPLICANT: Zapata, Gerardo A.
```

```

: TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
: TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
: NUMBER OF SEQUENCES: 72
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/121,952A
: FILING DATE: 24-Jul-1998
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/074330
: FILING DATE: 22-JAN-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/075467
: FILING DATE: 20-FEB-1998
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: P1085R4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5530
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 68:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8120 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: US-09-121-952A-68
```

Query Match

```
81.1%; Score 1082.6; DB 4; Length 8120;
Best Local Similarity 88.6%; Pred. No. 2.4e-248;
Matches 1210; Conservative 0; Mismatches 119; Indels 36; Gaps 2;
```

```
QY 1 GAGGTGCAGCTGTGGTGGAGGCTTGGTAAAGCCCGGGGCTCCCTTAGACTC 60
Db 1363 GAAGTTCAGCTAGTGCAGTCTGGCGTGGCTGGTGCAGCCAGGGGGTCTACTCCGTTG 1422
QY 61 TCTGTGACGTAGCGGATTCACCTTCACTGGCTACTGGATGTCCTGGGTCCGCGAGCT 120
Db 1423 TCTGTGACGTCTGGCTACTCTTCTGAGTCACTATATGCTGCTGCTGCTGCTGCTGCTG 1482
QY 121 CCAGGGAAGGGCTCGAGTGGGTGCTGAATTTAGATTGAATCTGATAATTTATCAACA 180
Db 1483 CCGGTAAAGGCTGGAATGGTTGATATTT-----GATCCTTCCAAATGGTGAAT 1536
QY 181 CATTTAGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTAGA 240
Db 1537 ACGTATAATCAAAAGTTCAGGGCGGTTTCACTTTTCTCGGACAACTCCAAAACACA 1596
QY 241 CTGTATCTCAAAATCAACAGCCTGAAACCCAGGAGCAGCGGTGTATTTACTGTACA --- 297
Db 1597 GCATACCTGCAGATGAACAGCCTGCTGCTGAGGACACTGCGTCTATTTACTGTGCAAGA 1656
QY 298 -----GATTTCTAGACTGGGCGCAGGAACTAGTCTC 330
Db 1657 GGGGATTATCGTCAATGGTGAATTTCTTCGACGTCTGGGGTCAAGGAACCTTGCTC 1716
QY 331 ACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCAGCCTCTCTCCAAG 390
Db 1717 ACCGTCTCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCAGCCTCTCTCCAAG 1776
QY 391 AGCACTCTGGGGGACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCCGAACCG 450
```

[illegible]

RESULT 8
US-09-234-340A-68
: Sequence 68, Application US/09234340A
: Patent No. 6468532
: GENERAL INFORMATION:
: APPLICANT: Genentech, Inc., Hsei, Vanessa
: APPLICANT: Koumenis, Iphigenia
: APPLICANT: Leong, Steven R.
: APPLICANT: Presta, Leonard G.

APPLICANT: Shahrokh, Zahra
 APPLICANT: Zapata, Gerardo A.
 TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
 TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/234, 340A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/121,952
 FILING DATE: 24-Jul-1998
 APPLICATION NUMBER: 60/074330
 FILING DATE: 22-JAN-1998
 PRIOR APPLICATION DATA: 60/075467
 APPLICATION NUMBER: 60/075467
 FILING DATE: 20-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,659
 REFERENCE/DOCKET NUMBER: P1085R4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5530
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 68:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8120 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 US-09-234-340A-68

2

```
Db 1717 ACCGTCCTCGGCTCCACCAAGGGCCCTCGTCTCCCGCTGGCACCCTCTCCAAG 1776
QY 391 AGCACCCTGTGGGGACAGCGGCGCTGGGTGCTGTGAAGACTACTTCCCGCAACCG 450
Db 1777 AGCACCCTGTGGGGACAGCGGCGCTGGGTGCTGTGAAGACTACTTCCCGCAACCG 1836
QY 451 GTGCGGTGTGTGAAGCTCAGGGCGCTGTGACAGCGCGCTGTGACACATTCCTCGGGTGTG 510
Db 1837 GTGCGGTGTGTGAAGCTCAGGGCGCTGTGACAGCGCGCTGTGACACATTCCTCGGGTGTG 1896
QY 511 CTACAGTCTCAGGACTACTCTCTCAGCAGCGTGTGACCGTGCCTCCACAGCTTG 570
Db 1897 CTACAGTCTCAGGACTACTCTCTCAGCAGCGTGTGACCGTGCCTCCACAGCTTG 1956
QY 571 GGCACCCAGACCTACATCTGCAAGGTGAATCACAAGCCCAAGCAGCACAAGGTGGACAAG 630
Db 1957 GGCACCCAGACCTACATCTGCAAGGTGAATCACAAGCCCAAGCAGCACAAGGTGGACAAG 2016
QY 631 AAAGTGGAGCCCAATCTTGTGACAAACTCACAATGCGCCACCGTCCCGCAGCACTGAA 690
Db 2017 AAAGTGGAGCCCAATCTTGTGACAAACTCACAATGCGCCACCGTCCCGCAGCACTGAA 2076
QY 691 CTCGCGGGGACCGCTCAGTCTCTCTCTCCCGCCCAAAACCCCAAGAGCACCCCTCATGATC 750
Db 2077 CTCCTGGGGGACCGCTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2136
QY 751 TCCCGGACCCCTGAGGTACATGCGTGTGTGTGACGTGAGCCAGCAAGACCTTGAGTGC 810
Db 2137 TCCCGGACCCCTGAGGTACATGCGTGTGTGTGACGTGAGCCAGCAAGACCTTGAGTGC 2196
QY 811 AAGTTCAACTGTAGTGTGAGCGGTGTGAGTGCATATGCAAGACAAAGCCCGGGAG 870
Db 2197 AAGTTCAACTGTAGTGTGAGCGGTGTGAGTGCATATGCAAGACAAAGCCCGGGAG 2256
QY 871 GAGCAGTACACAGCACGTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 930
Db 2257 GAGCAGTACACAGCACGTACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2316
QY 931 CTGAATGGCAAGGAGTACAAGTGTCAAGTGTCCCAACAAAGCCCTCCAGCCCGCCATCGAG 990
Db 2317 CTGAATGGCAAGGAGTACAAGTGTCAAGTGTCCCAACAAAGCCCTCCAGCCCGCCATCGAG 2376
QY 991 AAAACATCTCCAAAGCAAGGGCAGCGCCGAGAACACAGGTGTACACCCCTGCCCGCA 1050
Db 2377 AAAACATCTCCAAAGCAAGGGCAGCGCCGAGAACACAGGTGTACACCCCTGCCCGCA 2436
QY 1051 TCCCGGATGAGTGTACCAAGAACACAGTGTACGCTGACCTGCTGTGTGTGTGTGTGTGTGTGT 1110
Db 2437 TCCCGGATGAGTGTACCAAGAACACAGTGTACGCTGACCTGCTGTGTGTGTGTGTGTGTGTGT 2496
QY 1111 CCCAGGACATCGCGTGTGAGTGTGAGGAGCAATGGCGAGCGGAGAACAACTACAAGACC 1170
Db 2497 CCCAGGACATCGCGTGTGAGTGTGAGGAGCAATGGCGAGCGGAGAACAACTACAAGACC 2556
QY 1171 AGCCCTCCCGTGTGAGTGTGAGGAGCAATGGCGAGCGGAGAACAACTACAAGACC 1230
Db 2557 AGCCCTCCCGTGTGAGTGTGAGGAGCAATGGCGAGCGGAGAACAACTACAAGACC 2616
QY 1231 AAGAGCAGTGTGAGCAGGAGCAATGTCTCTCATGCTCCCGTGTGATGAGGCTCTGCAC 1290
Db 2617 AAGAGCAGTGTGAGCAGGAGCAATGTCTCTCATGCTCCCGTGTGATGAGGCTCTGCAC 2676
QY 1291 AACCCTACACGAGCAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1335
Db 2677 AACCCTACACGAGCAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2721
```

RESULT 9

US-09-049-672A-21

; Sequence 21, Application US/09049672A

; Patent No. 6135941

; GENERAL INFORMATION:

```
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guebler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1655 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGTUT11
; CLONE: 2747531
; US-09-049-672A-21
```

Query Match 79.98; Score 1066.4; DB 3; Length 1655;
Best Local Similarity 88.28; Pred. No. 1.1e-244; Mismatches 136; Indels 24; Gaps 2;
Matches 1192; Conservative 0;

```
QY 2 AGGTGCAGCTGTGTGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
Db 105 AGGTCCAGTTGTTACAGTCTGGGCTGAGGTGAAGAGCCTGGGGCTCAGTGCAGGTCT 164
QY 62 CTTGTGCAGCTAGCGATTCTTTCAGTGTCTGATGCTCTGGTTCGGCCAGGCTC 121
Db 165 CTTGCACGTTTCCGGATTCCCTCAGTGAATTTATCCGTGCAGTGGTGGCAGAGCTC 224
QY 122 CAGGGAAGGGCTCAGTGGGTTGCTGAAATAGATTGAAATCTGATAATATGCAACAC 181
Db 225 CTGGACAGGGCTTCAGTGGATGGAG-----GTTTAGCTCTGAAATGGAGGCGAG 278
QY 182 ATTATGGCGAGTCTGTGAAGGGGAAATTCACCTCTCAAGAGATGATTCAAAATCTAGAC 241
Db 279 TCTAGCAGAGAAATTCCTGGCAGACTCACCTTGTCCGAGGACACACTCTGCAGACACAG 338
QY 242 TGTATCTCAAAATGAACAGCCTGAAACCCGAGGACACAGCGCTGATTACTGTACA---- 297
Db 339 CCTACATGTTTCTGAACAACCTAGGATCTGAGGACTCGGCCATCTATTACTGTCAAGAC 398
QY 298 -----GATTTTCATAGACTGGGCCGAGGGAACACTAGTCAACCGCTCTCTCTCAG 343
```

Db	399	AAACATTACGATTTTCTTCGACTTCTGGGCGCAGGGACAATGTCTACCGTCTTTCAG	458
Qy	344	CTTCACCAAGGCGCATGGTCTTCCCTCGCAGCCCTCTCCAAAGACACCTCTGGGG	403
Db	459	CCTCCACCAAGGCGCATGGTCTTCCCTCGCAGCCCTCTCCAAAGACACCTCTGGGG	518
Qy	404	GCACAGGCGCCTGGGTGCTGCTCAAGGACTTCTCCCGGAAACGGGTGAGGGTGTGCT	463
Db	519	GCACAGGCGCCTGGGTGCTGCTCAAGGACTTCTCCCGGAAACGGGTGAGGGTGTGCT	578
Qy	464	GGAACCTCAGGCGCCTGACACAGCGGGGTGACACACTTCTCCCGGCTGTCTACAGTCTCTAG	523
Db	579	GGAACCTCAGGCGCCTGACACAGCGGGGTGACACACTTCTCCCGGCTGTCTACAGTCTCTAG	638
Qy	524	GACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCTCCAGCAGCTTGGGACCCAGACCT	583
Db	639	GACTCTACTCCCTCAGCAGCGTGTGACCGTGCCTCTCCAGCAGCTTGGGACCCAGACCT	698
Qy	584	ACATCTGCAAGCTGAATCACAAGCCCGCAGCAACACCAAGGTGGACAAAGTGGAGCCCA	643
Db	699	ACATCTGCAAGCTGAATCACAAGCCCGCAGCAACACCAAGGTGGACAAAGTGGAGCCCA	758
Qy	644	AATCTGTGACAAACTCAGCATGCCCACCGTGCCTCCAGCAGCTGACCTGCGGGGGCAC	703
Db	759	AATCTGTGACAAACTCAGCATGCCCACCGTGCCTCCAGCAGCTGACCTGCGGGGGCAC	818
Qy	704	CGTCAGTCTTCTCTTCCCGCCCAAAACCCAGGACACCCCTCATGATCTCCCGGACCCCTG	763
Db	819	CGTCAGTCTTCTCTTCCCGCCCAAAACCCAGGACACCCCTCATGATCTCCCGGACCCCTG	878
Qy	764	AGGTCACATGCGGTGGTGGACGTGAGCCACGACGACCCCTGAGTCAAGTCAACTGCT	823
Db	879	AGGTCACATGCGGTGGTGGACGTGAGCCACGACGACCCCTGAGTCAAGTCAACTGCT	938
Qy	824	ACGTGGAGCGGTGAGGTGCTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACA	883
Db	939	ACGTGGAGCGGTGAGGTGCTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAACA	998
Qy	884	GCACGTACCGTGTGCTCAGCGCTCTCACCGTCTCTGACACGAGGACTGGCTGAATGGCAAG	943
Db	999	GCACGTACCGTGTGCTCAGCGCTCTCACCGTCTCTGACACGAGGACTGGCTGAATGGCAAG	1058
Qy	944	AGTACAAGTGAAGGTCTTCCAAAGCCCTCCAGCCCTCCAGCCCTCCAGAAACCATCTCCA	1003
Db	1059	AGTACAAGTGAAGGTCTTCCAAAGCCCTCCAGCCCTCCAGCCCTCCAGAAACCATCTCCA	1118
Qy	1004	AAAGCAAGGCGCGGAGAACACAGAGTGTACACCCCTGCCCCATCCCGGGGATGAGC	1063
Db	1119	AAAGCAAGGCGCGGAGAACACAGAGTGTACACCCCTGCCCCATCCCGGGGAGAGA	1178
Qy	1064	TGACCAAGAACACAGGTGACGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1123
Db	1179	TGACCAAGAACACAGGTGACGCTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1238
Qy	1124	CCGTGGAGTGGAGAGCAATGGGAGCCGAGAGACAACTACAAGCCACCGCTCCCGTGC	1183
Db	1239	CCGTGGAGTGGAGAGCAATGGGAGCCGAGAGACAACTACAAGCCACCGCTCCCGTGC	1298
Qy	1184	TGGACTCCGACGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1243
Db	1299	TGGACTCCGACGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1358
Qy	1244	AGCAGGGGAACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1303
Db	1359	AGCAGGGGAACCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1418
Qy	1304	AGAGAGCCCTCTCCCTGTCTCCGGTAAATGA	1335
Db	1419	AGAAGAGCCCTCTCCCTGTCTCCCGGTAATGA	1450
RESULT 10			

US-08-286-740-3
; Sequence 3, Application US/08286740
; Patent No. 5561053
; GENERAL INFORMATION:
; APPLICANT: Crowley, Craig W.
; TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING
; TITLE OF INVENTION: HOST CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,740
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6557 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-286-740-3

Query Match 79.7%; Score 1063.4; DB 1; Length 6557;
Best Local Similarity 88.3%; Pred. No. 8.3e-244;
Matches 1205; Conservative 0; Mismatches 121; Indels 39; Gaps 3;

Qy	1	GAGGTGCAGCTGGTGGAGCTTGGGGGAGGCTTGGTAAGCCCGGGGGTCCCTTACGATC	60
Db	1363	GAAGTTCAGCTGGTGGAGCTTGGCGGTGGCTGGCAGCCAGGGGGCTCACCTCCGTTTG	1422
Qy	61	TCCTGTGCAGCTAGCGGATTCACCTTTCACCTTTCACCTTTCACCTTTCACCTTTC	117
Db	1423	TCCTGTGCAGCTTTCGCTACTCTCCATCACCTCCGGATATAGCTGGAACCTGATCCG	1482
Qy	118	GCTCCAGGAAAGGGCTCGAGTGGGTTCGTAATTTAGATTGAATCTGATATATGCA	177
Db	1483	GCCCCGGGTAAAGGCTTGGATGGTTGC-----ATCGATTAGCTATGCGGATCG	1533
Qy	178	ACACATTTAGCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATCAAAATCT	237
Db	1534	ACTAATAACCCCTAGGCTCAAGGGCGGTATCATATAAGTCGCGACGATTCACAAAC	1593
Qy	238	AGACTGTATCTGCAATCAACAGCTGAAACCGAGACACAGCCGTGTATTACTGTAC-	296
Db	1594	ACATTCTACCTGCAGATGAACAGCCTGGTCTGAGGACACTGCCGCTTATTATTGCT	1653
Qy	297	-----AGATTTATAGACTGGGGCCAGGGAACACTAGTC	330
Db	1654	CGAGGACGCCACTATTTCGGGCGCTTGGCACTTCGCGGTGGGGTCAAGAAACCTGTC	1713
Qy	331	ACCGTCTCTAGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCTCTCTCAAG	390


```
Db 1714 ACCGTCCTCTCGGCTCCACCAAGGCCCCATCGGCTTCCCGCTGGCACCCCTCTCTCCAAAG 1773
QY 391 AGCACCTCTGGGGGACACGCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCG 450
Db 1774 AGCACCTCTGGGGGACACGCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGCAACCG 1833
QY 451 GTGACGGTGTCTGGAACTCAGCGCCCTGACACGCGGCTGCACACCTTCCCGGCTGTC 510
Db 1834 GTGACGGTGTCTGGAACTCAGCGCCCTGACACGCGGCTGCACACCTTCCCGGCTGTC 1893
QY 511 CTACAGTCTCTAGGACTACTTCCCTCAGCAGCGTGGTACCGTGCCTCAGCAGCTTG 570
Db 1894 CTACAGTCTCTAGGACTACTTCCCTCAGCAGCGTGGTACCGTGCCTCAGCAGCTTG 1953
QY 571 GGCACCCAGACCTTACATCTGCAACGTGAATCACAAGCCGACCAACCAAGGTGACACAG 630
Db 1954 GGCACCCAGACCTTACATCTGCAACGTGAATCACAAGCCGACCAACCAAGGTGACACAG 2013
QY 631 AAGTGGAGCCCAAACTTGTGACAAAATCACAATGCCACCGTGCCTCCAGCAGCTGAA 690
Db 2014 AAGTGGAGCCCAAACTTGTGACAAAATCACAATGCCACCGTGCCTCCAGCAGCTGAA 2073
QY 691 CTCGGGGGGACCGTCACTCTTCTTCCCCCAAAACCAAGACACCCCTCATGATC 750
Db 2074 CTCGGGGGGACCGTCACTCTTCTTCCCCCAAAACCAAGACACCCCTCATGATC 2133
QY 751 TCCCGGACCCCTGAGTCACTGCTGCTGCTGAGTGGAGTGGAGCCACGAAGACCCCTGAGTGC 810
Db 2134 TCCCGGACCCCTGAGTCACTGCTGCTGAGTGGAGTGGAGCCACGAAGACCCCTGAGTGC 2193
QY 811 AAGTTCACTGCTGAGTGGAGCGGCTGGAGTGCATATGCAAGACAAAGCCGCGGAG 870
Db 2194 AAGTTCACTGCTGAGTGGAGCGGCTGGAGTGCATATGCAAGACAAAGCCGCGGAG 2253
QY 871 GAGCAGTACAAGACGCTACCGTGTGTCAGCGTCTCTCAGCGTCTCTGCAACGAGACTGG 930
Db 2254 GAGCAGTACAAGACGCTACCGTGTGTCAGCGTCTCTCAGCGTCTCTGCAACGAGACTGG 2313
QY 931 CTGAATGGCAAGGAGTACAAAGTGCAGAGTCTCCAAAGCCCTCCAGCCCGCATCGAG 990
Db 2314 CTGAATGGCAAGGAGTACAAAGTGCAGAGTCTCCAAAGCCCTCCAGCCCGCATCGAG 2373
QY 991 AAACCATCTCAAAGCCAAAGGAGCGCCGAGACCCGAGAACCAACGAGTGTACACCTGCCCCA 1050
Db 2374 AAACCATCTCAAAGCCAAAGGAGCGCCGAGACCCGAGAACCAACGAGTGTACACCTGCCCCA 2433
QY 1051 TCCCGGAGTGAAGTACCAAGAACCAAGTGCAGCGTCTCTGCTGCTCAAGGCTTCTAT 1110
Db 2434 TCCCGGAGTGAAGTACCAAGAACCAAGTGCAGCGTCTCTGCTGCTCAAGGCTTCTAT 2493
QY 1111 CCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGGCGAGCCGAGAACCAACTACAAGACC 1170
Db 2494 CCCAGCGACATCGCCGTGGAGTGGAGAGCAATGGGCGAGCCGAGAACCAACTACAAGACC 2553
QY 1171 AGCCTCCCGTGTGAGTCCGAGCGCTCTTCTTCTTCTACAGCAAGCTCACCGTGGAC 1230
Db 2554 AGCCTCCCGTGTGAGTCCGAGCGCTCTTCTTCTTCTACAGCAAGCTCACCGTGGAC 2613
QY 1231 AAGAGCAGTGGCAGCAGGGAACGCTTCTCTATGCTCCGTGATCATGAGGCTCTGAC 1290
Db 2614 AAGAGCAGTGGCAGCAGGGAACGCTTCTCTATGCTCCGTGATCATGAGGCTCTGAC 2673
QY 1291 AACCCTACACGACAGAGCCCTCTCTCTGCTCCGGGTAAATGA 1335
Db 2674 AACCCTACACGACAGAGCCCTCTCTCTGCTCCGGGTAAATGA 2718
```

RESULT 11

PCT-US95-09576-3
; Sequence 3, Application PC/TUS9509576
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; TITLE OF INVENTION: METHOD FOR SELECTING HIGH-EXPRESSING

; TITLE OF INVENTION: HOST CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09576
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286740
; FILING DATE: 05-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 798PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6557 bases
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; PCT-US95-09576-3

Query Match 79.7%; Score 1063.4; DB 5; Length 6557;
Best Local Similarity 88.3%; Pred. No. 8.3e-244;
Matches 1205; Conservative 0; Mismatches 121; Indels 39; Gaps 3;
QY 1 GAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTAAAGCCGGGGGCTCCCTTAGACTC 60
Db 1363 GAAGTTTCACTGTGTGGAGTCTGGCGTGGCTGTCAGCCAGGGGGCTCATCCGCTTG 1422
QY 61 TCCTGTGCAGCTACCGGATTCACCTTCA---GTGGCTACTGGATGCTCTGGTCCGCCAG 117
Db 1423 TCCTGTGCAGTTCCTGGCTACTCCATCACCTCCGGATATAGCTGGAACTGGATCCGTCAG 1482
QY 118 GCTCCAGGAAGGGCTCGAGTGGTTCGTAATAGATTGAAATCTGATATTATGCA 177
Db 1483 GCCCGGGTAAGGCCCTGGATGGGTGC-----ATCGATTAGTATGCCGGATCG 1533
QY 178 ACACATTATGCGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCT 237
Db 1534 ACTAATAATAACCTAGCGTCAAGGCGGTATCACTATAAGTCGCGACGATTCAAAAC 1593
QY 238 AGACTGTATCTGCAAAATGAACAGCTCAAAACCCAGACACACCCGCTGTATTACTGTAC- 296
Db 1594 ACATTCTACCTGCAGATGAACAGCTCGGTGCTGAGACACTGCGCTCTATTATTGTGCT 1653
QY 297 -----AGATTTCATAGACTGGGGCCAGGGAACACTAGTC 330
Db 1654 CGAGGCAGCCACTATTTCGGGCGCTGGCACTTCGCCCGTGTGGGTCAAGGAACCTGGTC 1713
QY 331 ACCGTCTCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCCTCTCTCAAG 390
Db 1714 ACCGTCTCTCGGCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCCTCTCTCAAG 1773
QY 391 AGCACCTCTGGGGGACACGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGCAACCG 450
Db 1774 AGCACCTCTGGGGGACACGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGCAACCG 1833

```
QY 451 GTGAGGTTGTCGTGGAACCTCAGCGCCCTGACAGAGCGGTGCACACCTTCCCGGCTGTC 510
Db 1834 GTGAGGTTGTCGTGGAACCTCAGCGCCCTGACAGAGCGGTGCACACCTTCCCGGCTGTC 1893
QY 511 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCAGCAGCTTG 570
Db 1894 CTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCGTCCCTCAGCAGCTTG 1953
QY 571 GGCACCCAGACCTACATCTGCAAGCTGAATCACAAGCCCAAGCAACACCAAGGTGGACAAG 630
Db 1954 GGCACCCAGACCTACATCTGCAAGCTGAATCACAAGCCCAAGCAACACCAAGGTGGACAAG 2013
QY 631 AAAGTGGAGCCCAATCTTGTGCAAAACTCACACATGCCACCGTCCCGCAGCACCTGAA 690
Db 2014 AAAGTGGAGCCCAATCTTGTGCAAAACTCACACATGCCACCGTCCCGCAGCACCTGAA 2073
QY 691 CTCGCGGGGCGACGCTCAGTCTTCTCTTCCCGCCAAACCCCAAGGACACCCCTCATGTC 750
Db 2074 CTCGCGGGGCGACGCTCAGTCTTCTCTTCCCGCCAAACCCCAAGGACACCCCTCATGTC 2133
QY 751 TCCCGGACCCCTGAGTGCATGCTGCTGGTGGTGGACGTGAGCCAGCAAGACCCCTGAGGTC 810
Db 2134 TCCCGGACCCCTGAGTGCATGCTGCTGGTGGTGGACGTGAGCCAGCAAGACCCCTGAGGTC 2193
QY 811 AAGTTCAACTGGTACGTGGAGCGGTGAGGTGCATATGCAAGACAAAGCCGCGGGAG 870
Db 2194 AAGTTCAACTGGTACGTGGAGCGGTGAGGTGCATATGCAAGACAAAGCCGCGGGAG 2253
QY 871 GAGCAGTACAACAGCAGCTACCGTGTGTGTCAGCGTCTCACCCTGCTGACCAAGGACTGG 930
Db 2254 GAGCAGTACAACAGCAGCTACCGTGTGTGTCAGCGTCTCACCCTGCTGACCAAGGACTGG 2313
QY 931 CTGAATGCAAGGAGTACAAGTGAAGTCTCCCAACAAAGCCCTCCAGCGCCCGCATCGAG 990
Db 2314 CTGAATGCAAGGAGTACAAGTGAAGTCTCCCAACAAAGCCCTCCAGCGCCCGCATCGAG 2373
QY 991 AAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGCAACAGGTGTACACCTGCCGCCCA 1050
Db 2374 AAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGCAACAGGTGTACACCTGCCGCCCA 2433
QY 1051 TCCCGGGATGAGTGCACCAAGAACAGGTGACGTGACCTGCCCTGCTCAAGGCTTCTAT 1110
Db 2434 TCCCGGGATGAGTGCACCAAGAACAGGTGACGTGACCTGCCCTGCTCAAGGCTTCTAT 2493
QY 1111 CCCAGCAGATCGCGTGGAGTGGAGAGCAATGGGAGCCGCGGAGCAACACTACAAGACC 1170
Db 2494 CCCAGCAGATCGCGTGGAGTGGAGAGCAATGGGAGCCGCGGAGCAACACTACAAGACC 2553
QY 1171 ACGCTCCCGTGTGAGTCCGACGGCTCTCTTCTTCTACAGCAAGCTCACCGTGGAC 1230
Db 2554 ACGCTCCCGTGTGAGTCCGACGGCTCTCTTCTTCTACAGCAAGCTCACCGTGGAC 2613
QY 1231 AAGAGCAGTGGCAGCAGGGAAGCTTCTCTATGCTCCGCTGATGATGAGGCTCTGCAC 1290
Db 2614 AAGAGCAGTGGCAGCAGGGAAGCTTCTCTATGCTCCGCTGATGATGAGGCTCTGCAC 2673
QY 1291 AACCACACGCAAGACAGCCTCTCCCTCTCCCGGGTAAATGA 1335
Db 2674 AACCACACGCAAGACAGCCTCTCCCTCTCCCGGGTAAATGA 2718
```

RESULT 12

```
US-08-378-939-9
; Sequence 9, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESS: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
```

```
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: GDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 35..92
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 93..1465
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 35..1465
; US-08-378-939-9
```

Query Match 78.1%; Score 1042.6; DB 2; Length 1617;

Best Local Similarity 86.6%; Pred. No. 4.9e-234; Mismatches 134; Indels 51; Gaps 2;

Matches 1194; Conservative 0;

```
QY 2 AGTGCAGCTGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
Db 93 AGATGCAGGTGGTGCAGTCTGGGGCTGAAGTAAAGAGCCTGGTCTCGGTGACGGTCT 152
QY 62 CTTGTGCAGCTAGCGGATTCACTTTTCAGTGGCTACTGGATGTCCTGGTCCGCCAGGCTC 121
Db 153 CTTGCAAGCATCTGGAGGCACCTTTCAGCACTATGCTATCAGCTGGGTGCGACAGGCC 212
QY 122 CAGGGAAGGGCTCGAGTGGTGTGTAATAGATTGAAATCTGTAATATGTAACAC 181
Db 213 CTGGACAAGGGCTTGAGTGGTGGGAG-----GGATATCCCTCTTTTGGTACACAA 266
QY 182 ATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAATCTAGAC 241
Db 267 CCTACTCAGAACTTCCAGGGCAGAGTACCGATTACCGCGGACAAATCCACCACACAG 326
QY 242 TGTATCTGCAATGAAACAGCCTGAAACCGAGGACACAGCCGTGTATTACTGTACAG--- 298
Db 327 CCACATGGAGCTGACTAGCCTGAGATCTGAGGACACAGCCGCTGTATTACTGTGCGACAG 386
QY 299 -----ATTTTCATAGACTGGGCC 316
Db 387 ATCGCTACAGGAGGCAAAATTTTGACCGGGCCCGGGTGGCTGGTTTCGACCCCTGGGCC 446
QY 317 AGGGAACACTAGTACCGCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG 376
```

Db 447 AGGCGACCCCTGTGTCACCGCTCTCCTCAGCCTCCACCAAGGGCCATCGGTCTTCCCCCTGG 506
Qy 377 CACCTCTCCCAAGACCACTCTGGGGCAGACGGCCCTGGGCTGCTGTCAAGGACT 436
Db 507 CACCTCTCTCCCAAGACCACTCTGGGGCAGACGGCCCTGGGCTGCTGTCAAGGACT 566
Qy 437 ACTTCCCGCAACCGGTGAGCGGTGCTGTGAACCTCAGGCGCCCTGACACGCGCGGTGCACA 496
Db 567 ACTTCCCGCAACCGGTGAGCGGTGCTGTGAACCTCAGGCGCCCTGACACGCGCGGTGCACA 626
Qy 497 CTTTCCCGGCTCTCTACAGTCTCCTCAGGACTCTACTCCTCAGCAGCGTGTGACCGTGC 556
Db 627 CTTTCCCGGCTCTCTACAGTCTCCTCAGGACTCTACTCCTCAGCAGCGTGTGACCGTGC 686
Qy 557 CTTTCCCGGCTCTCTACAGTCTCCTCAGGACTCTACTCCTCAGCAGCGTGTGACCGTGC 616
Db 687 CTTTCCCGGCTCTCTACAGTCTCCTCAGGACTCTACTCCTCAGCAGCGTGTGACCGTGC 746
Qy 617 CCAAGGTGACAAAGAAAGTGGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCGT 676
Db 747 CCAAGGTGACAAAGAAAGTGGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCGT 806
Qy 677 GCGCAGCAGCTGAATCGGGGGGACCGTCACTGCTTCTTCCCGCCCAAAACCGCAAG 736
Db 807 GCGCAGCAGCTGAATCGGGGGGACCGTCACTGCTTCTTCCCGCCCAAAACCGCAAG 866
Qy 737 ACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCTGCTGTGACGTGACGTGACCGACG 796
Db 867 ACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCTGCTGTGACGTGACGTGACCGACG 926
Qy 797 AAGACCTGAGGTCAAGTTCAACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGTCA 856
Db 927 AAGACCTGAGGTCAAGTTCAACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGTCA 986
Qy 857 CAAAGCGCGGAGGAGGAGTCAACAGCAGTACCGTACCGTACCGTACCGTACCGTACCGT 916
Db 987 CAAAGCGCGGAGGAGGAGTCAACAGCAGTACCGTACCGTACCGTACCGTACCGTACCGT 1046
Qy 917 TGCACGAGGCTGGCTGAATGCAAGGAGTCAACGAGTCAACGAGTCAACGAGTCAACGAGTCA 976
Db 1047 TGCACGAGGCTGGCTGAATGCAAGGAGTCAACGAGTCAACGAGTCAACGAGTCAACGAGTCA 1106
Qy 977 CAGCGCCCATCGAGAAACCACTCTCCAAAGCCAAAGGAGCGCCCGGAGAACCCACAGGTGT 1036
Db 1107 CAGCGCCCATCGAGAAACCACTCTCCAAAGCCAAAGGAGCGCCCGGAGAACCCACAGGTGT 1166
Qy 1037 ACACCTGCCCCCATCCCGGAGTGAATGCAAGGAGTCAACGAGTCAACGAGTCAACGAGTCA 1096
Db 1167 ACACCTGCCCCCATCCCGGAGTGAATGCAAGGAGTCAACGAGTCAACGAGTCAACGAGTCA 1226
Qy 1097 TCAAGGCTTCTTATCCCGAGGAGTCAACGAGTCAACGAGTCAACGAGTCAACGAGTCAACG 1156
Db 1227 TCAAGGCTTCTTATCCCGAGGAGTCAACGAGTCAACGAGTCAACGAGTCAACGAGTCAACG 1286
Qy 1157 ACACTTACAAGACCAACCGCTCCCGTGTGAGTCAACGAGTCAACGAGTCAACGAGTCAACG 1216
Db 1287 ACACTTACAAGACCAACCGCTCCCGTGTGAGTCAACGAGTCAACGAGTCAACGAGTCAACG 1346
Qy 1217 AGCTCAGCTGACAGAGGAGTCAACGAGTCAACGAGTCAACGAGTCAACGAGTCAACGAGTCA 1276
Db 1347 AGCTCAGCTGACAGAGGAGTCAACGAGTCAACGAGTCAACGAGTCAACGAGTCAACGAGTCA 1406
Qy 1277 ATGAGGCTCTGACACCACTACAGCAGGAGGAGTCAACGAGTCAACGAGTCAACGAGTCAACG 1335
Db 1407 ATGAGGCTCTGACACCACTACAGCAGGAGGAGTCAACGAGTCAACGAGTCAACGAGTCAACG 1465

RESULT 13

US-08-487-550-11

; Sequence 11, Application US/08487550

; Patent No. 6113898

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; -LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; NAME/KEY: mat_peptide
; LOCATION: 1..1431
; US-08-487-550-11

Query Match 77.9%; Score 1040.6; DB 3; Length 1431;
Best Local Similarity 86.9%; Pred. No. 14e-238;
Matches 1199; Conservative 0; Mismatches 129; Indels 51; Gaps 3;
Qy 2 AGGTGCAGCTGGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
Db 59 AGGTGCAGCTGCAGGAGTCCGGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCCTCA 118
Qy 62 CCTGTGCAG---CTAGCGGATTCACTTTCAGTGGCTACTGGATGTCTTGGGTCCGCAGG 118
Db 119 CCTCGCTGTCTCTGTGGCTTCCATCAGCGGTGGTTATGGCTGGGGTGGATCCGCAGC 178
Qy 119 CTCCAGGGAAGGGCTCGAGTGGGTGCTGAAATTCATTGAATTCGATTAATATGCA 178
Db 179 CCCAGGGAAGGGCTCGAGTGGATTC-----GGATTTCTATAGTAGTAGTGGGACA 232
Qy 179 CACATTATGGGAGTCTGTGAAGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTA 238
Db 233 CCTACTACAACCCCTCCCTCAAGAGTCAAGTCAACATTTCAACAGACACGTCCTCAAGAAC 292
Qy 239 GACTGTATCTCAATGAACACCTGAAACCCGAGGACACGCGTGTATTACTGT---- 294
Db 293 AGTTCTCCCTGAAGCTGAACCTTATGACCGCGCGGACACGCGGTGTATTACTGTGTGA 352
Qy 295 -----ACAGATTTTCATAGACTGGGCGC 316
Db 353 GAGATCGCTTTTTTTCAGTTGTGTGAATGTTTACACAACTGTTTCGATGTCTGGGGCC 412
Qy 317 AGGGAACACTAGTCACCGCTCTCCCTCAGCCTCCACCAAGGCCCATCGGTCTTCCCGCTGG 376
||||| ||| ||||||||||||||| |||||||||||||||||||

Db 413 CGGAGTCTCGTTCACCGTCTCTCCTCAGCTAGCACCAAGGGCCCAATCGGTCTTCCCCCTGG 472
Qy 377 CACCTCTCTCAAGACACCTCTTGGGGGCACAGGGCCCTGGGTGCTGGTCAAGACT 436
Db 473 CACCTCTCTCAAGACACCTCTTGGGGGCACAGGGCCCTGGGTGCTGGTCAAGACT 532
Qy 437 ACTTCCCGGAACCGGTGACGGTGTCTGGTGAACCTCAGGGCCCTGACACAGGGGTGACAA 496
Db 533 ACTTCCCGGAACCGGTGACGGTGTCTGGTGAACCTCAGGGCCCTGACACAGGGGTGACAA 592
Qy 497 CTTTCCCGGTCTCTACAGTCTCAGAGCTCTACTCCCTCAGCAGCGTGTGACCGTGC 556
Db 593 CTTTCCCGGTCTCTACAGTCTCAGAGCTCTACTCCCTCAGCAGCGTGTGACCGTGC 652
Qy 557 CCTCAGAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAAGCA 616
Db 653 CCTCAGAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAAGCA 712
Qy 617 CCAAGGTGGACAAGAAAGTGGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCGT 676
Db 713 CCAAGGTGGACAAGAAAGTGGAGCCCAATCTTGTGACAAAACCTCACACATGCCACCGT 772
Qy 677 GCCAGCACCTGAACCTCGCGGGGCACCGTCAGTCTTCTCTTCCCCCAAAACCCCAAGG 736
Db 773 GCCAGCACCTGAACCTCGCGGGGCACCGTCAGTCTTCTCTTCCCCCAAAACCCCAAGG 832
Qy 737 ACACCTCATGATCTCCGGACCCCTGAGGTACATCGGTGGTGGAGCTGAGCCACG 796
Db 833 ACACCTCATGATCTCCGGACCCCTGAGGTACATCGGTGGTGGAGCTGAGCCACG 892
Qy 797 AAGACCTGAGGTCAAGTTCAACTTGAAGTGGAGCGGTGGAGGTGAGGTGATGCAATGCCAAG 856
Db 893 AAGACCTGAGGTCAAGTTCAACTTGAAGTGGAGCGGTGGAGGTGAGGTGATGCAATGCCAAG 952
Qy 857 CAAAGCCCGGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTCAAGCTCTCACCGTCC 916
Db 953 CAAAGCCCGGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTCAAGCTCTCACCGTCC 1012
Qy 917 TGCACAGGACTGCTGTAATGGCAAGGAGTACAAGTCAAGTGTCAACAAAGCCCTCC 976
Db 1013 TGCACAGGACTGCTGTAATGGCAAGGAGTACAAGTGTCAACAAAGCCCTCC 1072
Qy 977 CAGCCCATCGAAGAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCCAGAGTGT 1036
Db 1073 CAGCCCATCGAAGAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCCAGAGTGT 1132
Qy 1037 ACACCTGCCCCATCCCGGGATGAGCTGACCAAGAACCCAGGTGAGCTGACCTGCTGG 1096
Db 1133 ACACCTGCCCCATCCCGGGATGAGCTGACCAAGAACCCAGGTGAGCTGACCTGCTGG 1192
Qy 1097 TCAAGGCTTCTATCCAGCGACATCCCGGTGGAGTGGGAGAGCAATGGGCGAGCGGAGA 1156
Db 1193 TCAAGGCTTCTATCCAGCGACATCCCGGTGGAGTGGGAGAGCAATGGGCGAGCGGAGA 1252
Qy 1157 ACAACTACAAGCACCGCTCCCGTGTGGACTCCGAGCGCTCTCTCTCTCTACAGCA 1216
Db 1253 ACAACTACAAGCACCGCTCCCGTGTGGACTCCGAGCGCTCTCTCTCTCTACAGCA 1312
Qy 1217 AGCTCACCGTGGACAAGAGCAGTGGGAGCAGGGGAACGCTTCTCTATGCTCCGTGATGC 1276
Db 1313 AGCTCACCGTGGACAAGAGCAGTGGGAGCAGGGGAACGCTTCTCTATGCTCCGTGATGC 1372
Qy 1277 ATGAGGCTCTGCACAACCACTACAGCAGAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1335
Db 1373 ATGAGGCTCTGCACAACCACTACAGCAGAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1431

RESULT 14

US-08-793-450-7
; Sequence 7, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA

APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHAABIRI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA USA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793.450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24.618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1418
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..57
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..1418
OTHER INFORMATION: /product= "IMMUNOGLOBIN, HEAVY
OTHER INFORMATION: CHAIN"
US-08-793-450-7
Query Match 77.9%; Score 1039.8; DB 4; Length 1418;
Best Local Similarity 86.7%; Pred. No. 2.2e-238;
Matches 1187; Conservative 0; Mismatches 137; Indels 45; Gaps 2;
Qy 2 AGTGCAGCTGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTAGACTCT 61
Db 59 AGGTCCAACTGGAGCAGTGGGGCGCAGGACTCTTGAAGCCTTCGGAGACCCCTGTCCCTCA 118
Qy 62 CCTGTGCACGTAGCGATTTCATTTTCAGTGGCTACTGGATGCTCTGGGTCCGCCAGGCTC 121
Db 119 CTGTCACTCTATGTGGGTCTTTCAGTGGTACTTACTGGAGCTGGATCCGCCAGCCCC 178
Qy 122 CAGGGAAGGGCTCGAGTGGGTTCGTAATTTAGATTGAAATCTGATAATTATGCAACAC 181
Db 179 CAGGGAAGGGCTGGAGTGGATTGGGAATCA-----ATCATAGTGAAGCACCA 229
Qy 182 ATTATCGGAGTCTGTGAAGGGGAATTCACCATCTCAAGAGATGATTCAAATCTAGAC 241
Db 230 ACTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCACCAAGAACCA 289

QY	242	TGATCTCGAATGAACAGCCGTGAAACCGAGGACACAGCCGTGTATTACTHGTACAGATT	301
Db	290	TCCTCCTGAAACTGTGTGACGGCGCGAGCACAGCGTGTGTATTATTCTTGCTGAGAGG	349
QY	302	TCATAGA-----CTGGGGGCCAGGAAACAC	325
Db	350	CCCCAGAGTATANTGGAAGTATCATGGGGACTGTTTCGACCCTCTGGGGCCCAAGGTACCA	409
QY	326	TAGTCACCGTCTCTCAGCCTCCACAAGGGCCCATFCGTCTTCCCTCGTGCACCCCTCC	385
Db	410	CTGTCACCGTCTCCTCAGCCTCCACAAGGGCCCATFCGTCTTCCCTCGTGCACCCCTCC	469
QY	386	CBAAGAGACCTCTGGGGGCACAGGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGG	445
Db	470	CCAAGAGCACCTCTGGGGGCACAGGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGG	529
QY	446	AACCGGTGACGGTTCGTGGAACCTCAGGCGCCCTCACCAGCGGGTGACACACCTTCCCGG	505
Db	530	AACCGGTGACGGTTCGTGGAACCTCAGGCGCCCTCACCAGCGGGTGACACACCTTCCCGG	589
QY	506	CTGTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTTCCACGA	565
Db	590	CTGTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCTTCCACGA	649
QY	566	GCTTGGGACCCAGACTACATCTGCAAGGTGAATCAAGCCGAGCAACACCAAGGTGG	625
Db	650	GCTTGGGACCCAGACTACATCTGCAAGGTGAATCAAGCCGAGCAACACCAAGGTGG	709
QY	626	ACAAGAAAGTGGAGCCCAATCTGTGACAAAACCTCACACATGCCACCGTGCCACGAC	685
Db	710	ACAAGAAAGTGGAGCCCAATCTGTGACAAAACCTCACACATGCCACCGTGCCACGAC	769
QY	686	CTGAACTTCGGGGGACCGTTCAGTCTTCTCTTCCCGCCAAAAACCCAAAGGACACCCCTCA	745
Db	770	CTGAACTCTCTGGGGGACCGTTCAGTCTTCTCTTCCCGCCAAAAACCCAAAGGACACCCCTCA	829
QY	746	TGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCTGAGCCACGAAGACCCCTG	805
Db	830	TGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCTGAGCCACGAAGACCCCTG	889
QY	806	AGGTCAAGTTCAACTGCTACGTGGAGGGGTGGAGTGCATAATGCCAAGAACAAAGCCGC	865
Db	890	AGGTCAAGTTCAACTGCTACGTGGAGGGGTGGAGTGCATAATGCCAAGAACAAAGCCGC	949
QY	866	GGGAGGACGAGTACACAGCAGTACCGTGTGGTCAGGGTCTCTCACCGTCTCTGCACCCAGG	925
Db	950	GGGAGGACGAGTACACAGCAGTACCGGCTGCTCAGCGTCTCTCAAAGTCTCTGCACCCAGG	1009
QY	926	ACTGGCTGAATGGCAAGGAGTACAGTGCAGGTTCTCAACAAAGCCCTCCCGAGCCGCCA	985
Db	1010	ACTGGCTGAATGGCAAGGAGTACAGTGCAGGTTCTCAACAAAGCCCTCCCGAGCCGCCA	1069
QY	986	TCGAGAAAACATCTCAAAGCCAAAGGSCACGCCGAGAACACACAGTGTACACCTGTC	1045
Db	1070	TTGAGAAACCATCTCCAAGCCAAAGGSGACGCCCGAGAACCCACAGGTGTACACCTGTC	1129
QY	1046	CCCCATCCCGGGTAGCTGACCAAGAACGAGGTGAGCCTGACCTGCTGGTCAAAAGCT	1105
Db	1130	CCCCATCCCGGGTAGCTGACCAAGAACGAGGTGAGCCTGACCTGCTGGTCAAAAGCT	1189
QY	1106	TCATATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCGAGCCGGAGAACCAACTACA	1165
Db	1190	TCATATCTAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCGAGCCGGAGAACCAACTACA	1249
QY	1166	AGACCAGGCTCCCGTGCTGGACTCCGAGCGGCTCTTCTTCTCTACAGCAAGCTCACCG	1225
Db	1250	AGACCAGGCTCCCGTGCTGGACTCCGAGCGGCTCTTCTTCTCTACAGCAAGCTCACCG	1309
QY	1226	TGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGATGATGAGCTC	1285
Db	1310	TGGACAAGAGCAGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGATGATGAGCTC	1369
QY	1286	TGCACAACCACTACACGCAAGAGAGCGCTCTCCCTGCTTCCCGGGTAAATG	1334

Db	1370	TGCAACACCTACAGCAGAGACCTCTCCTGCTGTCTCGGGTAATG	1418
RESULT 15			
US-08-149-099C-3			
; Sequence 3, Application US/08149099C			
; Patent No. 5736137			
GENERAL INFORMATION:			
; APPLICANT: ANDERSON, Darrell R.			
; APPLICANT: HANNA, Nabil			
; APPLICANT: LEONARD, John E.			
; APPLICANT: NEWMAN, Roland A.			
; APPLICANT: REFF, Mitchell E.			
; APPLICANT: RASTETTER, William H.			
; TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AN			
; TITLE OF INVENTION: RADIOLABELLED ANTIBODIES TO HUMAN B LYM			
; TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATM			
; TITLE OF INVENTION: LYMPHOMA			
; NUMBER OF SEQUENCES: 9			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS			
; STREET: P.O. Box 1404			
; CITY: Alexandria			
; STATE: Virginia			
; COUNTRY: United States			
; ZIP: 22313-1404			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patentin Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/149,099C			
; FILING DATE: 03-NOV-1993			
; CLASSIFICATION: 424			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 07/978,891			
; FILING DATE: 12-NOV-1992			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Teskin, Robin L.			
; REGISTRATION NUMBER: 35,030			
; REFERENCE/DOCKET NUMBER: 012712-014			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (703) 836-6620			
; TELEFAX: (703) 836-2021			
; INFORMATION FOR SEQ ID NO: 3:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 9209 base pairs			
; TYPE: nucleic acid			
; STRANDEDNESS: single			
; TOPOLOGY: circular			
; MOLECULE TYPE: DNA (genomic)			
; HYPOTHETICAL: NO			
; ANTI-SENSE: NO			
US-08-149-099C-3			
Query Match 77.9%; Score 1039.8; DB 1; Length 9			
Best Local Similarity 86.8%; Pred. No. 3.8e-238;			
Matches 1181; Conservative 0; Mismatches 147; Indels			
Qy	2	AGGTGACGCTGTGTGGAGTCTGGGGAGGCTTGGTAAAGCCCGGGGGTCCCTTGA	1418
Db	2459	AGGTACACTGCAGCAGCGCTGGGGCTGACCTGGTGAGCCTGGGGCCTCAGTGA	1418
Qy	62	CCTGTGCAGCTACGGCGATTCACTTTTCAGTGGCTACTGGATGCTCTGGGTCGCGC	1418
Db	2519	CCTGCAAGCCTTCTCGCTACACATTTACCAGTTACAATATGACATCGGTGGTAAAC	1418
Qy	122	CAGGAAGCGGCTCAGTGGTGTGCTGAATAGATTGAATCTGATAATATGAT	1418
Db	2579	CTGGTTCGGGCTCGAATGGATGGATGGAGCTATT-----TATCCGGAATGGTG	1418

Qy	182	ATTATGCGGAGTCTGTGAAGGGGAAATTCACCATCTCAAGAGATGATTCAAAATCTTAGAC	241
Db	2633	CCTACAATCAGAGTGTCAAAGGCAAGGCCACATTTGACTGCGACAGAAATCTCTCCAGCACAG	2692
Qy	242	TGTATCTGCAAAATGAACAGAGCTGAAACCGAGGACACAGCGTGATTACTGTACA----	297
Db	2693	CCTACATGCACTCAGCAGCGCTGCATCTGTGAGGACTCTGCGGTCTATTACTGTGCAAGAT	2752
Qy	298	-----GATTTTCATAGACTGGGGCCAGGGAAACACTAGTCAACCG	334
Db	2753	CGACTTACTACGGCGGTGACTGGTACTTCAATGCTCTGGGCGCAGGACCAACGCTCACCG	2812
Qy	335	TCCTCTCAGCCTCCACAAGGGCCCATGGTCTTCCCTCTGGCACCCTCTCTCCAAGAGCA	394
Db	2813	TCTCTGCACTAGCACCAAGGGCCCATGGTCTTCCCTCTGGCACCTCTCTCCAAGAGCA	2872
Qy	395	CCTCTGGGGCACAGCGGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGGAACGGGTGA	454
Db	2873	CCTCTGGGGCACAGCGGCCCTGGGTGCTGGTCAAGGACTACTTCCCGAACCGGTGA	2932
Qy	455	CGGTGTCGTGGAACTCAGGGGCCCTGCACAGCGGGCTGCACACCTTCCCGGCTGTCTCTAC	514
Db	2933	CGGTGTCGTGGAACTCAGGGGCCCTGACCAGCGGGCTGCACACCTTCCCGGCTGTCTCTAC	2992
Qy	515	AGTCTCAGGACTTACTCCTCTCAGCAGGTGTCACCGTGCCTCTCAGCAGCTTGGGCA	574
Db	2993	AGTCTCAGGACTTACTCCTCTCAGCAGGTGTCACCGTGCCTCTCAGCAGCTTGGGCA	3052
Qy	575	CCCAGACTACATCTCTCAACGTGAATCAACAGCCAGCAACCAAGGTGACAAAGAAAG	634
Db	3053	CCCAGACTACATCTCTCAACGTGAATCAACAGCCAGCAACCAAGGTGACAAAGAAAG	3112
Qy	635	TGGAGCCCAATCTGTGACAAACTCACATGCCACCGTGCCTGCCAGCAGCTTGAACTCG	694
Db	3113	CAGAGCCCAATCTGTGACAAACTCACATGCCACCGTGCCTGCCAGCAGCTTGAACTCG	3172
Qy	695	CGGGGGCACCGTCAGTCTTCTCTTCCCCCAAAACCCAGGACACACCTCATGATCTCCC	754
Db	3173	TGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCCAGGACACACCTCATGATCTCCC	3232
Qy	755	GGACCCCTGAGGTACATCGTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTCAGGT	814
Db	3233	GGACCCCTGAGGTACATCGTGGTGGAGCTGAGCCACGAAGACCCCTGAGGTCAGGT	3292
Qy	815	TCAACTGGTACGTGGAGCGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGC	874
Db	3293	TCAACTGGTACGTGGAGCGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGC	3352
Qy	875	AGTACACACGACTACCGTGTGGTCAGGTCCTCAGCGTCTCCACCGTCTCCACAGGACTGCTGA	934
Db	3353	AGTACACACGACTACCGTGTGGTCAGGTCCTCAGCGTCTCCACCGTCTCCACAGGACTGCTGA	3412
Qy	935	ATGGCAAGAGTACAAGTCCAAGGTCTCCAACAAAGCCCTCCACAGCCCCCATCGAAGAAA	994
Db	3413	ATGGCAAGAGTACAAGTCCAAGGTCTCCAACAAAGCCCTCCACAGCCCCCATCGAAGAAA	3472
Qy	995	CCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAAGGTGTACACCTGCCCCCATCCC	1054
Db	3473	CCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAAGGTGTACACCTGCCCCCATCCC	3532
Qy	1055	GGATGAGCTGACCAAGAACCAAGGTGAGCTGACCTGCCTGGTCAAGGGCTTCTATCCCA	1114
Db	3533	GGATGAGCTGACCAAGAACCAAGGTGAGCTGACCTGCCTGGTCAAGGGCTTCTATCCCA	3592
Qy	1115	GCACATCGCCCGTGGAGTGGGAGACAATGGCGAGCCGGAGAACCAACTACAAGCACCGC	1174
Db	3593	GCACATCGCCCGTGGAGTGGGAGACAATGGCGAGCCGGAGAACCAACTACAAGCACCGC	3652
Qy	1175	CTCCCGTGTGGACTCCGAGCGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGA	1234
Db	3653	CTCCCGTGTGGACTCCGAGCGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGA	3712
Qy	1235	GCAGGTGGCAGCAGGGGAACTGCTTCTCATGCTCGGTGATGCATGAGGCTCTGCACAAAG	1294